Functional Coupling of T1Rs and T2Rs by Gi Proteins and Cell-Based Assays For The Identification of T1R and T2R Modulators

Priority Information

[0001] This application claims benefit of priority to U.S. Provisional Serial No. 60/457,318 filed March 26, 2003 and U.S. Serial No. 60/444,172 filed on February 3, 2003. Both of these applications are incorporated by reference in their entireties herein.

Field of the Invention

[0002] The present invention relates to novel methods and materials for the identification of modulators, *e.g.,* enhancers, agonists and antagonists of G protein-coupled receptors (GPCRs) involved in taste, i.e., T1Rs and T2Rs. These modulators may be used as flavor-affecting additives, e.g., in foods, beverages and medicines for human or animal consumption. More specifically, the present invention provides MAP Kinase, cAMP and adenylyl cyclase cell-based assays for the identification of modulators of GPCRs involved in taste modulation, *i.e.,* T2Rs and T1Rs, preferably human T1Rs and T2Rs.

[0003] Further, the invention provides cell based assays, *e.g.,* MAP Kinase, cAMP accumulation and adenylyl cyclase cell-based assays that rely on the discovery that G proteins other than gustducin and promiscuous and pernicious, G proteins such as $G\alpha_{15}$, *i.e.,* G_i proteins functionally couple to T1Rs and T2Rs and use $G\alpha i$ to transmit signals to downstream effectors.

Background of the Invention

[0004] The family of receptors that transmit signals through the activation of heterotrimeric GTP binding proteins (G proteins) constitutes the largest group of cell surface proteins involved in signal transduction. These receptors participate in a broad range of important biological functions and are implicated in a number of disease states. More than half of all drugs currently available influence GPCRs. These receptors affect the generation of small molecules that act as intracellular mediators or second messengers, and can regulate a highly interconnected network of biochemical routes controlling the activity of several members of the mitogen-activated protein kinase (MAPK) superfamily.

[0005] In fact, the activation of members of the mitogen-activated protein kinase (MAPK) family represents one of one of the major mechanisms used by eukaryotic cells to transduce extracellular signals into cellular responses (J. Blenis, Proc. *Natl. Acad. Sci.,* USA 90:5889 (1993) **(1)**; Blumer et al., *TIBS* 19:236 (1994) **(2)**; Cano et al., *TIBS* 20:117 (1995) **(3)**; Seger et al., *FASEB J.* 9:726 (1995) **(4)**: R.J. Davis, *TIBS* 19:470 (1994) **(5)**). The MAPK superfamily consists of the p42 (ERK2)/p44 (ERK1) MAPKs and the stress-activated protein kinases, c-Jun N-terminal kinase (JNK) and p38 MAPK. (Robinson and Dickenson, Eur. *J. Pharmacol.* 413(2-3):151-61 (2001)**(6)**).

[0006] Mitogen-activated protein kinase (MAPKs) (also called extracellular signal-regulated kinases or ERKs) are rapidly activated in response to ligand binding by both growth factor receptors that function as tyrosine kinases (such as the epidermal growth factor (EGF) receptor) and receptors that are complexed

with heterodimeric guanine nucleotide binding proteins (G proteins) such as the thrombin receptor. In addition, receptors like the T cell receptor (TCR) and B cell receptor (BCR) are non-covalently associated with src family tyrosine kinases which activate MAPK pathways. Specific cytokines like tumor necrosis factor (TNFalpha) can also regulate MAPK pathways. The MAPKs appear to integrate multiple intracellular signals transmitted by various second messengers. MAPKs phosphorylate and regulate the activity of enzymes and transcription factors including the EGF receptor, Rsk 90, phospholipase A_2, c-Myc, c-Jun and EIK-1/TCF. Although the rapid activation of MAPKs by tyrosine kinase receptors is dependent on Ras, G protein-mediated activation of MAPK also occurs through pathways dependent and independent of Ras.

[0007] Particularly, it is known that the activation of MAP/ERK kinase which is induced by GPCRs involves both of the G alpha and G beta gamma subunits and further involves a common signaling pathway with receptor-tyrosine-kinases. (Lopez-llasaca, *Biochem. Pharmacol.* 56(3): 269-77 (1998) **(7)**). For example, the G protein beta gamma subunit has been shown to activate Ras, Raf and MAP kinase in HEK293 cells. (Ito et al., *FEBS* Lett. 368(1): 183-7 (1995) **(8)**).

[0008] Additionally of relevance to the present invention, within the last several years, a number of groups including the present assignee Senomyx Inc., have reported the identification and cloning of genes from two GPCR families that are involved in taste modulation and have obtained experimental results that provide a greater understanding of taste biology. These results indicate

that bitter, sweet and amino acid taste, also referred as umami taste, is triggered by activation of two types of specific receptors located at the surface of taste receptor cells (TRCs) on the tongue *i.e.*, T2Rs and T1Rs **(9-11)** (Gilbertson et al., *Corr. Opin. Neurobiol.,* 10(4):519-27 (2000); Margolskee, RF, *J. Biol. Chem.* 277(1):1-4 (2002); Montmayeur et al., *Curr. Opin. Neurobiol.*, 12(4):366-71 (2002)). It is currently believed that at least 26 and 33 genes encode functional receptors (T2Rs) for bitter tasting substances in human and rodent respectively **(11-13)** (Montmayeur et al., *Curr. Opin. Neurobiol.*, 12(4):366-71 (2002); Adler et al., *Cell* 100(6):693-702 (2000); Matsunami et al., *Nature* 404(6678):601-4 (2000)). By contrast there are only 3 T1Rs, T1R1, T1R2 and T1R3, which are involved in umami and sweet taste **(14-16)** (Li et al., *Proc. Natl Acad Sci., USA* 99(7):4692-6 (2002); Nelson et al., *Nature* (6877):199-202 (2002); Nelson et al., *Cell* 106(3):381-96 (2001)). Structurally, the T1R and T2R receptors possess the hallmark of G protein-coupled receptors (GPCRs), *i.e.,* 7 transmembrane domains flanked by small extracellular and intracellular amino- and carboxyl-termini respectively.

[0009] T2Rs which have been cloned from different mammals including rats, mice and humans **(12)** (Adler et al., *Cell* 100(6): 611-8 (2000)). T2Rs comprise a novel family of human and rodent G protein-coupled receptors that are expressed in subsets of taste receptor cells of the tongue and palate epithelia. These taste receptors are organized in clusters in taste cells and are genetically linked to loci that influence bitter taste. The fact that T2Rs modulate bitter taste has been demonstrated in cell-based assays. For example, mT2R-5, hT2R-4 and mT2R-8 have been shown to be activated by bitter molecules in in vitro gustducin assays,

providing experimental proof that T2Rs function as bitter taste receptors. **(80)** (Chandrasheker et al., *Cell* 100(6): 703 (2000)).

[0010] The present assignee has filed a number of patent applications relating to various T2R genes and the corresponding polypeptides and their use in assays, preferably high-throughput cell-based assays for identifying compounds that modulate the activity of T2Rs. These Senomyx applications i.e., U.S. Serial No. 09/825,882, filed on April 5, 2001, U.S. Serial No. 191,058 filed July 10, 2002 and U.S. Provisional Application Serial No. 60/398,727, filed on July 29, 2002 all incorporated by reference in their entireties herein. Additionally, the present assignee has exclusively licensed patent applications relating to T2R genes which were filed by the University of California i.e., U.S. Serial No. 09/393,634, filed on September 10, 1999 (recently allowed) and U.S. Serial No. 09/510,332, filed February 22, 2000, that describe various mouse, rat and human T2R sequences and the use thereof in assays for identifying molecules that modulate specific T2Rs and which modulate (enhance or block) bitter taste. These applications and the sequences contained therein are also incorporated by reference in their entireties herein.

[0011] Further, the present assignee and its exclusive licensor, the University of California, have filed a number of patent applications relating to human and rodent T1R taste receptors. Specifically, Senomyx has filed patent applications 09/897,427, filed on July 3, 2001, U.S. Serial No. 10/179,373, filed on June 26, 2002, and U.S. Serial No. 09/799,629, filed on March 7, 2001, all of which and the sequences contained therein are incorporated by reference in their entirety

herein. Additionally, the University of California has filed a number of applications exclusively licensed by Senomyx including U.S. Serial No. 09/361,631, filed July 27, 1999, now U.S. Patent No. 6,383,778, issued on May 7, 2002 and U.S. Serial No. 09/361,652, filed on July 27, 1999, which relates to cloned rat, mouse and human T1R1 and T1R2 genes and the use of the genes and corresponding polypeptides to identify T1R modulators. These University of California applications and the sequences contained therein are also incorporated by reference in their entirety herein.

[0012] The three T1R gene members T1R1, T1R2 and T1R3 form functional heterodimers that specifically recognize sweeteners and amino acids **(14-16) (**Li et al., *Proc. Natl Acad Sci., USA* 99(7):4692-6 (2002); Nelson et al., *Nature* (6877):199-202 (2002); Nelson et al., *Cell* 106(3):381-96 (2001)). Functional studies performed in HEK293 cells expressing the promiscuous G protein $G\alpha_{15/16}$, also disclosed therein have shown that the rodent and human T1R2/T1R3 combination recognizes natural and artificial sweeteners **(14-16) (**Li et al., *Proc. Natl Acad Sci., USA* 99(7):4692-6 (2002); Nelson et al., *Nature* (6877):199-202 (2002); Nelson et al., *Cell* 106(3):381-96 (2001)) while the rodent and human T1R1/T1R3 combination recognizes several L-amino acids and monosodium glutamate (MSG), respectively **(14, 15) (**Li et al., *Proc. Natl Acad Sci., USA* 99(7):4692-6 (2002); Nelson et al., *Nature* (6877):199-202 (2002)). These results, demonstrate that T1Rs are involved in sweet and umami taste.

[0013] Particularly, the co-expression of T1R1 and T1R3 in recombinant host cells results in a hetero-oligomeric taste receptor that responds to umami taste

stimuli. Umami taste stimuli include by way of example monosodium glutamate and other molecules that elicit a "savory" taste sensation. By contrast, the co-expression of T1R2 and T1R3 in recombinant host cells results in a hetero-oligomeric sweet taste receptor that responds to both naturally occurring and artificial sweeteners. As with T2Rs, T1R DNAs and the corresponding polypeptides have significant application in cell and other assays, preferably high throughput assays, for identifying molecules that modulate T1R taste receptors; particularly the T1R2/T1R3 receptor (sweet receptor) and the T1R1/T1R3 receptor (umami receptor). T1R modulators can be used as flavor-affecting additives in foods, beverages and medicines.

[0014] The patents and patent application referenced above, which are incorporated by reference in their entirety herein, disclose a number of assay methods, including cell-based high throughput screening assays for identifying T1R and T2R agonists and antagonists. However, notwithstanding what is disclosed therein, novel and improved assays for identifying T1R and T2R agonists and antagonists are still needed. In particular other high throughput assays that provide for the rapid and accurate identification of T1R or T2R agonists and antagonists would be beneficial. Also, a greater understanding of what conditions and materials yield functional T1Rs and T2Rs and assays based on this greater understanding would further be beneficial.

Objects of the Invention

[0015] Toward that end, it is an object of the invention to provide a greater understanding of the means by which T1Rs and T2Rs functionally couple to G proteins and their signaling pathways.

[0016] More particularly, it is an object of the invention to identify G proteins other than $G\alpha_{15}$ and gustducin (G_i proteins) which functionally couple to GPCRs involved in taste, *i.e.*, T1Rs and T2Rs.

[0017] It is specifically an object of the invention to provide assays, preferably cell-based assays which exploit the discovery that T1Rs and T2Rs functionally couple to G_i proteins, *e.g.* $G\alpha_i$.

[0018] Thus, it is an object of the invention to provide cell-based assays for identifying T1R and T2R modulators that use techniques which assay the effect of putative modulator on $G\alpha_i$ signaling pathways.

[0019] It is a more specific object of the present invention to provide cell-based assays for identifying T1R and T2R modulators that use techniques which assay the effect of a putative T1R or T2R modulator on at least one of MAPK activity, cAMP accumulation and adenylyl cyclase activity.

[0020] More specifically, it is an object of the invention to provide novel cell-based assays for identifying T1R and T2R agonists or antagonists or enhancers that modulate MAPK activation independent of PLC activation.

[0021] It is another specific object of the invention to provide cell-based assays for identifying T1R and T2R modulators that use techniques which assay the effect of said putative modulators on $G\alpha_i$ signaling pathways that affect downstream effectors including but not exclusive to cAMP and MAPK.

[0022] It is another specific object of the invention to provide cell-based assays for identifying T1R or T2R modulators comprising:

(i) contacting a eukaryotic cell that stably or transiently expresses at least one T1R or T2R and a G protein that functionally couples therewith, *e.g.*, Gαi with a putative T1R or T2R modulator compound;

(ii) assaying the effect of said putative modulator compound on at least one of MAPK activation, cAMP or adenylyl cyclase activity; and

(iii) identifying whether said compound is a T1R or T2R agonist, antagonist or allosteric modulator compound based on whether it modulates the amount of activated MAPK, intracellular levels of cAMP or adenylyl cyclase activity that is expressed by said eukaryotic cell.

[0023] It is another specific object of the invention to provide novel cell-based assays for identifying compounds that modulate the effect of a known T1R or T2R activating compound, e.g., a known sweetener, umami or bitter compound comprising:

(i) contacting a eukaryotic cell that stably or transiently expresses at least one T1R or T2R and a G protein that functionally couples

preferably thereto, *e.g.*, $G_{\alpha i}$, with a putative T1R or T2R modulator and with a compound that is known to activate at said least one T1R or T2R, wherein said compound and said putative agonist or antagonist compound are contacted with the eukaryotic cell separately or in combination;

(ii) assaying whether said putative modulator compounds affect at least one of MAPK activation, intracellular levels of cAMP or adenylyl cyclase activity expressed by said eukaryotic cell;

(iii) identifying whether said compound is a T1R or T2R modulator compound based on whether it results in a detectable change in activated MAPK, cAMP or adenylyl cyclase activity expressed by said eukaryotic cell.

[0024] In preferred embodiments of the invention, MAPK activation will be measured using polyclonal or monoclonal antibodies that specifically recognize activated forms of MAPK, *e.g.*, antibodies that specifically bind p42/p44 MAPK or p38 MAPK or will be measured using proximity assays (e.g., AlphaScreen™ from Packard or High Content Screening Systems (e.g., ERK, MAPK Activation HitKit™ from Cellomics).

[0025] Also, in preferred embodiments, cAMP levels are measured by immunoassay methods, optionally after cAMP accumulation is induced by the use of a compound such as forskolin.

[0026] It is a preferred object of the invention to use the subject cell-based assays, *e.g.*, MAPK, cAMP or adenylyl cyclase assays to identify compounds that themselves elicit sweet taste by activating the T1R2/T1R3 sweet receptor or

which modulate (enhance or inhibit (block)) sweet taste elicited by another compound that activates the T1R2/T1R3 sweet receptor such as saccharin, cyclamate, saccharin, D-tryptophan, monellin, xorbitol, xylitol, L-tryptophan, and other known sweeteners.

[0027] It is another preferred object of the invention to use the subject cell-based assays, preferably MAPK, cAMP or adenylyl cyclase assays to identify compounds that themselves elicit a bitter taste or which modulate (enhance or inhibit (block)) the bitter taste elicited by another compound that activates the particular T2R, e.g., cycloheximide, denotonium, quinine, lidocaine, etc.

[0028] It is another preferred object of the invention to use the subject cell-based preferably MAPK, cAMP or adenylyl cyclase assays to identify compounds that themselves elicit umami taste by activating the T1R1/T1R3 receptor or which modulate (enhance or block) umami taste elicited by another compound that activates the T1R1 /T1R3 umami receptor such as a glutamate or another savory amino acid containing compound, optionally in conjunction with inosine monophosphate.

[0029] It is another object of the invention to provide T2R or T1R agonists or antagonists identified using the subject cell-based assays that monitor the effects of a compound on $G_{\alpha i}$ mediated signaling pathways, *e.g.*, cAMP, MAPK and adenylyl cyclase assays.

[0030] It is still another object of the invention to use said T2R or T1R modulatory compounds as flavor-affecting additives, e.g., in foods, beverages and medicaments for human or animal consumption.

[0031] It is yet another object of the invention to produce compositions containing T2R or T1R modulatory compounds identified using the subject cell-based MAPK and cAMP assays.

[0032] It is a specific object of the invention to provide assays for identifying modulators of T1R or T2R taste receptors wherein at least one T1R to T2R is stably or transiently expressed in a cell preferably a mammalian cell line such as HEK-293, together with a G_i protein that functionally couples therewith, *e.g.*, $G\alpha_i$, and the modulator is identified based on its effect on $G\alpha_i$ mediated signaling pathways that affect the expression of downstream effectors such as cAMP, MAPK and adenylyl cyclase.

Detailed Description of Figures

[0033] **Figure 1** contains the results of an experiment showing that mT2R5 couples to activation of ERK1/2 MAPK. **Panel A** contains results of an experiment wherein mT2R5-expressing HEK293 cells were incubated with buffer alone (HBSS), 100 ng/mL EGF, 40 μM cycloheximide, 250 μM quinine, 2 mM denatonium, 2 mM saccharin, 100 mM sucrose, or 5 mM MSG/1mM IMP in HBSS for 5 minutes at 37°C. Cell lysate proteins were resolved by SDS-PAGE, transferred to nitrocellulose membranes and then blotted using antibodies directed against phosphorylated ERK1/2 MAPK. PTX-treated cells were incubated with 100 ng/mL PTX overnight prior to experiment. **Panel B** contains

an experiment that measured the course of cycloheximide-induced ERK1/2 phosphorylation in mT2R5-expressing cells. **Panel C** contains an experiment wherein HEK293 cells transiently expressing rT2R9 were treated as described in **Panel A.** **Panel D** contains an experiment showing the effect of increasing concentrations of cycloheximide on ERK1/2 activation. mT2R5-expressing HEK293 cells were incubated with cycloheximide diluted in HBSS (0.1 to 100 NM) for 5 minutes at 37°C. Cell lysate proteins were analyzed as described in **Panel A**. Bands (inset) were quantified and data were normalized to maximal stimulation of phospho-ERK1/2 MAPK (at 100 μM cycloheximide) **Panel E** contains an experiment wherein naive HEK293 cells were treated as described in **Panel A**. The results in **Panels A, D and E** are representative of at least 3 independent experiments. The results in **Panels B and C** are representative of two independent experiments.

[0034] **Figure 2** contains experiments which demonstrate that hT1R2/R3 and hT1R1/R3 couple to activation of ERK1/2 MAPK. **Panel A** contains an experiment wherein hT1R2/R3-expressing HEK293/G15 cells incubated with buffer alone (D-PBS), 100 ng/mL EGF, 40 μM cycloheximide, 250 μM quinine, 2 mM denatonium, 2 mM saccharin, 100 mM sucrose, 5mM MSG/7mM IMP, 4mM D-tryptophane and 10mM cyclamate in D-PBS for 5 minutes at 37°C. Cell lysate proteins were resolved by SDS-PAGE, transferred to nitrocellulose membranes and then blotted using antibodies directed against phosphorylated ERK1/2 MAPK. PTX-treated cells were incubated with 100 ng/mL PTX overnight prior to the experiment. **Panel B** contains an experiment wherein hTlR1/hT1R3-

expressing HEK293/G15 cells were treated with mifepristone to induce receptor expression (described *infra*) 48 hours later, cells were incubated with buffer alone (D-PBS), 100 ng/mL EGF, 40 μM cycloheximide, 250 μM quinine, 2 mM denatonium, 2mM saccharin, 100mM sucrose and 5mM MSG/1mM IMP in D-PBS for 5 minutes at 37°C. Cell lysate proteins were analyzed as described in **Panel A**. **Panel C** contains an experiment wherein naive HEK293/G15 cells were treated as described in **Panel B**. (Results therein are representative of at least 3 independent experiments).

[0035] **Figure 3** contains experiments showing the effects of increasing concentrations of sweeteners and MSG on ERK1/2 activation. **Panels A and B** contain experiments wherein hT1R2/hT1R3-expressing HEK293/G_{15} cells were incubated with increasing concentrations of either saccharin (**Panel A**) (0.078 to 10 mM) or sucrose (**Panel B**) (3.13 to 400 mM) for 5 minutes at 37°C. Cell lysate proteins were resolved by SDS-PAGE, transferred to nitrocellulose membranes and then blotted using antibodies directed against phosphorylated ERK1/2 MAPK. Bands (insets) were quantified and data were normalized to maximal stimulation of phospho-ERK1/2 MAPK (at 10 mM and 400 mM saccharin and sucrose respectively). **Panel C** contains an experiment wherein hTlRl/hT1R3-expressing HEK293/G15 cells were induced for receptor expression as described in the methods section (*infra*). Cells were then incubated with increasing concentrations of MSG (0.03 to 60 mM) in the absence or presence of 10 mM IMP for 5 minutes at 37°C. Cell lysate proteins were then analyzed as described in A. Bands (inset) were quantified and data were normalized to maximal stimulation

of phospho-ERK1/2 MAPK (at 10 mM and 60 mM MSG). These results are representative of at least three independent experiments.

[0036] **Figure 4** contains experiments which show that cycloheximide inhibits cAMP accumulation in mT2R5-expressing cells. **Panel A** contains an experiment wherein mT2R5-expressing HEK293 and naive HEK293 cells were incubated with 0.7 μM forskolin and 50 μM rolipram in the absence and presence of 40 μM cycloheximide in HBSS for 15 minutes at 37°C. cAMP levels were determined as described in the methods section *infra*. cAMP content of mT2R5-expressing cells stimulated with buffer (0.525% DMSO in HBSS) was 5 pmol/well. cAMP content of mT2R5-expressing cells stimulated with forskolin was 73 pmol/well. Cells were also treated with 100ng/ml PTX for 4 hours at 37°C and then stimulated as described above. Under these conditions the cAMP content of mT2R5-expressing cells stimulated with buffer (0.525% DMSO in HBSS) was 4 pmol/well and cAMP content of mT2R5-expressing cells stimulated with forskolin was 80 pmol/well. **Panel B** contains an experiment comparing the effect of increasing concentrations of cycloheximide on forskolin-induced cAMP accumulation. mT2R5-expressing HEK293 cells were incubated with 0.7 μM forskolin and 50 μM rolipram in the presence of cycloheximide diluted in HBSS (0.03 to 100 μM) for 15 minutes at 37°C and cAMP levels were determined as described in the methods section *infra*. Results in **Panel A** correspond to the mean +/-SD of three independent experiments performed in quadruplicates. Results in **Panel B** are representative of three similar experiments. In the figure, * means that the result is significantly different than forskolin response, $p < 0.05$.

[0037] **Figure 5** contains experiments indicating that sweeteners inhibit cAMP accumulation in hT1R2/hT1R3 expressing-cells. **Panel A** contains an experiment wherein hT1R2/hT1R3-expressing HEK293/G15 cells were incubated with 5 μM forskolin and 50 μM rolipram in the absence and presence of either 200mM fructose, 200mM sucrose, 1mM aspartame, 3mM cyclamate, 2mM saccharin or 50 μM monellin in D-PBS for 15 minutes at 37°C and cAMP levels were determined as described in the methods section. cAMP content of cells stimulated with buffer (0.525% DMSO in D-PBS) was 3 pmol/well. cAMP content of mT2R5-expressing cells stimulated with forskolin was 23 pmol/well. Cells were also treated with 100ng/ml PTX for 4 hours at 37°C and then stimulated as described above. Under these conditions, the cAMP content of cells stimulated with buffer (0.525% DMSO in D-PBS) was 4 pmol/well and cAMP content of cells stimulated with forskolin was 149 pmol/well. **Panel B** shows naive HEK293/G15 cells that were treated as in **Panel A**. Cells stimulated with buffer (0.525% DMSO in D-PBS) was 4 pmol/well and cAMP content of cells stimulated with forskolin was 90 pmol/well. **Panel C** contains an experiment comparing the effects of increasing concentrations of cyclamate on forskolin-induced cAMP accumulation. Cells were incubated with of 5 μM forskolin and 50 μM rolipram in the absence or presence of increasing concentrations of cyclamate (0.08 to 10 mM). cAMP content of cells stimulated with forskolin alone was 11 pmol/well. **Panel D** contains an experiment comparing the efects of increasing concentration of aspartame on forskolin-induced cAMP accumulation. Cells were incubated with of 5 μM forskolin and 50 μM rolipram in the absence or presence of increasing concentrations of

aspartame (0.03 to 4 mM). cAMP content of cells stimulated with forskolin alone was 14 pmol/well. **Panel E** contains an experiment comparing the effects of increasing concentration of saccharin on forskolin-induced cAMP accumulation. Cells were incubated with of 5 μM forskolin and 50 μM rolipram in the absence or presence of increasing concentrations of saccharin (0.008 to 1 mM). cAMP content of cells stimulated with forskolin alone was 24 pmol/well. Results in **Panels A and B** correspond to the mean +/- SD of three to six independent experiments performed in quadruplicates. Results in **Panels C-E** are representative of three similar experiments. In the figure, * means that the result was significantly different than the forskolin response, $p < 0.05$.

[0038] **Figure 6** contains experiments which demonstrate that MSG inhibits cAMP accumulation in hTlRl/hTlR3-expressing cells. hT1R1/hTlR3-expressing HEK293/G15 cells were induced for receptor expression as described in the methods section. (*infra*) Cells were incubated with 50 μM rolipram in the absence and presence of 3 mM MSG/10 mM IMP in D-PBS for 15 minutes at 37°C and cAMP levels were determined as described in the method section. cAMP content of cells in the presence of rolipram was 120 pmol/well. Cells were also treated with 100ng/ml PTX for 4 hours at 37°C and then stimulated as described above. Under these conditions cAMP content of hT1R1/hTlR3-expressing cells was 95 pmol/well. Results correspond to the mean +/- SD of three independent experiments performed in quadruplicates. In the figure, * means that the result was significantly different than the forskolin response, $p < 0.05$.

[0039] **Figure 7** contains experiments showing that mT2R5 and hT1R2/hT1R3 do not functionally couple to G_s. **Panel A** contains an experiment wherein hT1R2/hTlR3-expressing HEK293/G15 cells were incubated with 50 μM rolipram in the absence and presence of either 1mM aspartame, 3mM cyclamate, 2mM saccharin, 50 μM monellin and 10 μM isoproterenol in D-PBS for 15 minutes at 37°C and cAMP levels were determined as described in the methods section *infra*. Under these conditions basal level of cAMP was 2 pmol/well. **Panel B** contains an experiment wherein hT1R2/hT1R3-expressing cells were treated with 100ng/ml PTX for 4 hours at 37°C and then stimulated as described above. Under these conditions the basal level of cAMP was 1.3 pmol/well. **Panel C** contains an experiment wherein mT2R5-expressing HEK293 cells were incubated with 50 μM rolipram in the absence and presence of 40 μM cycoheximide or 10 μM isoproterenol in HBSS for 15 minutes at 37°C. Under these conditions basal level of cAMP was 5 pmol/well. Cells were also treated with 100ng/ml PTX for 4 hours at 37°C and then stimulated as described above. Under these conditions basal level of cAMP was 4 pmol/well. Results correspond to the mean +/- SD of three independent experiments performed in quadruplicates.

[0040] Figure 8 contains a schematic showing how $G\alpha_i$ is believed to complement α-gustducin signaling pathways in TRCs. Sweet and bitter receptors functionally couple to α-gustducin (thick arrows) **(10, 17)** Margolskee, RF, *J. Biol. Chem.* 277(1):1-4 (2002); Wong et al., *Nature* 381(6585): 796-800 (1996)). It is not known yet if the MSG (umami) receptor couples to α-gustducin

but our results point to $G\alpha_i$ as a strong candidate for its cognate G protein in TRCs. Alpha--gustducin is thought to directly couple to calcium mobilization via $G\beta\gamma$ and activation of PLCβ2 **(9, 10)** (Gilbertson et al., *Curr. Opin. Neurobiol.,* 10(4):519-27 (2000); Margolskee, RF, *J. Biol. Chem.* 277(1):1-4 (2002)) . Action of PLC-β2 produces two second messengers, inositol triphosphate (IP3) and diacylglycerol (DAG). IP3 triggers the release of calcium from intracellular stores. This event is not sufficient to fully depolarize TRCs **(18)** (Zhang et al., *Cell* 112(3):293-301 (2003)). DAG **(19)** or PLCβ2 activity itself **(18)** (Zhang et al., *Cell* 112(3):293-301 (2003)) may somehow activate a cell surface trp channel, TRPM5, leading to extracellular calcium influx in TRCs, followed by depolarization and ultimately taste perception. As disclosed in detail *infra*, the results of the present invention suggest that $G\alpha_i$ is capable of complementing α-gustducin function in TRCs. Indeed, PLCβ2 is known to be activated by the $G\beta\gamma$ subunit of G proteins belonging to the G_i family **(20-24)** (Li et al., *Science* 287(54-55):1046-9 (2000); Wu et al., *Proc. Natl Acad Sci., USA* 90(11):5297-5301 (1993); Katan, *Biochem Biophys. Acta* 1436(1-2):5-17 (1998); Smrcka et al., *J. Biol Chem.* 272(24):15045-48 (1993); Rhee et al., *J. Biol. Chem.* 272(24):15045-8 (1997)), and $G\alpha_{i1\text{-}2}$ are expressed in TRCs **(25, 26)** (Kusakabe et al., *Chem. Senses* 25(5):525-31 (2000); Asano-Miyoshi *Neurosci. Lett.* 283(1):64 (2000)). This alternative pathway could explain the residual responsiveness of α-gustducin-deficient mouse to bitter substances and sweeteners **(17, 27, 28)** (Wong et al., *Nature* 381(6585): 796-800 (1996); He et al., *Chem. Senses* 27(8):719-27 (2002); Ruiz-Avila et al., *Proc. Natl Acad Sci., USA* 98(15):2868-73 (2001)). Current models **(9, 10)** (Gilbertson et al., *Curr. Opin. Neurobiol.,* 10(4):519-27 (2000);

Margolskee, RF, *J. Biol. Chem.* 277(1):1-4 (2002)) also suggest that α-gustducin couples to the activation of a PDE leading to a decrease of cAMP in TRCs. It is not yet known how a-gustducin may activate PDE(s). The decrease of cAMP mediated by $G\alpha_i$ could also complement this signaling cascade. Modulation of cAMP levels in TRCs could have roles that are not yet fully defined such as defining the tone of paracrine transmission between TRCs **(29)** (Harness et al., *J. Physiol.* 543(Pt. 2):601-614 (2002)) and modulating gene expression through a balance between CREB and phosphorylated-CREB **(30)** (Cao et al., *Neuroreport* 13(10):1321-25 (2002)).

Detailed Description of the Invention

[0041] The present invention provides cell-based assays for identifying compounds that modulate, *e.g.*, enhance, agonize or antagonize the activity of specific T1R or T2R taste receptors or that modulate the effect of another T1R or T2R activator compound preferably by assaying their effect on the expression of an activated form of MAPK, cAMP levels or adenylyl cyclase activity by a eukaryotic cell that stably or transiently expresses at least one functional T1R or T2R. In its broadest embodiment, the cell-based assays encompass the identification of T1R or T2R modulator by detecting its effect on any $G_{\alpha i}$ associated signaling pathway.

[0042] The invention specifically provides cell-based assays that relate to the discovery that T1Rs and T2Rs both functionally couple to G proteins other than α-gustducin or $G\alpha_{15}$, particularly G_i proteins such as $G\alpha_i$. As discussed in detail *infra,* it has been shown that bitter compounds such as cycloheximide specifically

activate ERK1/2 mitogen activated kinases in cells expressing a T2R and $G\alpha_i$ and also that cycloheximide inhibits forskolin-induced cAMP accumulation. Further, it has been shown that natural and artificial sweetener compounds activate ERK1/2 in cells expressing hT1R2/hT2R13 and $G\alpha_i$, and that monosodium glutamate specifically activates ERK1/2 in cells expressing hT1R1/ht1R3 and $G\alpha_i$ protein and further completely inhibits forskolin-induced cAMP accumulation in such cells; and that activation of ERK1/2 by these compounds is totally abolished by treatment with pertussin toxin. These results provide compelling evidence that the T1R and T2R receptors indeed couple and activate ERK1/2 and inhibit adenylyl cyclase through $G\alpha_i$.

[0043] Thus, the invention provides cell-based assays for the identification of taste modulatory compounds that rely on these discoveries. These taste modulatory compounds have potential utility as flavor enhancers or flavor additives for incorporation in foods and beverages for human or animal consumption.

DEFINITIONS AND ABBREVIATIONS

[0044] Prior to providing a detailed description of the invention, and its preferred embodiments, the following definitions and abbreviations are provided. Otherwise all terms have their ordinary meaning as they would be construed by one skilled in the relevant art.

ABBREVIATIONS USED

[0045] Some abbreviations used in this application are set forth below.

[0046] cAMP: 3' 5'-cyclic adenosine monophsphate, TRCs: Taste receptor cells, GPCRs: G protein-coupled receptors, MSG: Monosodium glutamate, PDE: phosphodiesterase; MAPK: Mitogen activated protein kinase, IMP: inosine monophosphate, PTX: pertussis toxin, EGF: Epidermal growth factor, PKC: Protein kinase C, RTKs: Receptor tyrosine kinases, PKA: Protein kinase A, ACs: Adenylyl cyclases, cNMP: cyclic nucleotide monophosphate, CREB: cAMP response element-binding protein, PLCβ2: Phospholipase Cβ2, Trp: Transient receptor potential.

[0047] "Taste cells" include neuroepithelial cells that are organized into groups to form taste buds of the tongue, e.g., foliate, fungiform, and circumvallate cells (see, e.g., Roper et al., Ann. Rev. Neurosci. 12:329-353 (1989)) **(31)**. Taste cells are also found in the palate and other tissues, such as the esophagus and the stomach.

[0048] "T1R" refers to one or more members of a family of G protein-coupled receptors that are expressed in taste cells such as foliate, fungiform, and circumvallate cells, as well as cells of the palate, and esophagus *(see, e.g.,* Hoon *et* al., *Cell*, 96:541-551 (1999), **(32)** herein incorporated by reference in its entirety). The definition of "T1R" should further be construed based on DNA and amino acid sequences disclosed in the Senomyx and University of California patent applications and publications incorporated by reference herein. (*See e.g.,* **10-12**) Members of this family are also referred to as GPCR-B3 and TR1 in WO 00/06592 as well as GPCR-B4 and TR2 in WO 00/06593. GPCR-B3 is also herein referred to as rT1R1, and GPCR-B4 is referred to as rT1R2. Taste receptor cells

can also be identified on the basis of morphology *(see, e.g.,* **31**), or by the expression of proteins specifically expressed in taste cells. T1R family members may have the ability to act as receptors for sweet or umami taste transduction, or to distinguish between various other taste modalities. T1R sequences, including hT1R1, hT1R2 and hT1R3 are identified in the Senomyx and University of California patent applications incorporated by reference in their entirety herein and are provided *infra*, in an Appendix after the claims.

[0049] "T1R" nucleic acids encode a family of GPCRs with seven transmembrane regions that have "G protein-coupled receptor activity," e.g., they may bind to G proteins in response to extracellular stimuli and promote production of second messengers such as IP3, cAMP, cGMP, and Ca^{2+} via stimulation of enzymes such as phospholipase C and adenylate cyclase (for a description of the structure and function of GPCRs, *see, e.g.,* Fong, *TM Cells Signal.* 8(3):217-224 (1996) **(33)** and Baldwin, et al., *J. Mol. Biol.* 272(1):144-164 (1997) **(34)**. A single taste cell may contain many distinct T1R polypeptides.

[0050] The term "T1R" family therefore refers to polymorphic variants, alleles, mutants, and interspecies homologus that: (1) have at least about 35 to 50% amino acid sequence identity, optionally about 60, 75, 80, 85, 90, 95, 96, 97, 98, or 99% amino acid sequence identity to a T1R polypeptide, preferably those identified in the patent applications incorporated by reference herein, over a window of about 25 amino acids, optionally 50-100 amino acids; (2) specifically bind to antibodies raised against an immunogen comprising an amino acid sequence preferably selected from the group consisting of the T1R polypeptide

sequence disclosed in the patent applications incorporated by reference herein and conservatively modified variants thereof; (3) are encoded by a nucleic acid molecule which specifically hybridize (with a size of at least about 100, optionally at least about 500-1000 nucleotides) under stringent hybridization conditions to a sequence selected from the group consisting of the T1R nucleic acid sequences contained in the applications incorporated by reference in their entirety herein, and conservatively modified variants thereof; or (4) comprise a sequence at least about 35 to 50% identical to an amino acid sequence selected from the group consisting of the T1R amino acid sequence identified in the patent applications incorporated by reference in their entirety herein.

[0051] The term "T2R" refers to one or more members of a family of G protein coupled receptors that are expressed in taste cells, specifically, the tongue and palate epithelia. In particular, T2R includes the particular genes identified in the Senomyx and University of California applications relating to T2Rs incorporated by reference in their entirety herein. T2Rs are genetically linked to loci associated with bitter taste perception in mice and humans. More specifically, the term "T2R" and terms including T2R, *e.g.*, T2R04 or T2R05 refers generally to isolated T2R nucleic acids, isolated polypeptides encoded by T2R nucleic acids, and activities thereof. T2R nucleic acids and polypeptides can be derived from any organism. The terms "T2R" and terms including "T2R" also refer to polypeptides comprising receptors that are activated by bitter compounds, and to nucleic acids encoding the same. Thus both T1Rs and T2Rs

comprise different families of chemosensory GPCRs. Sequences of various T2Rs are also contained in the Appendix that precedes the claims.

[0052] G proteins are heterotrimeric proteins composed of a single α subunit complexed with the βγ dimer. Molecular cloning has resulted in the identification of 18 distinct .α. subunits, 5β subunits, and 12γ subunits. G proteins are usually divided into four subfamilies G_i, G_s, G_q, and G_{12} based on the sequence similarity of the Gα subunit. Several lines of evidence suggest that the interaction between a given GPCR and its cognate G protein involves multiple sites of contact on both proteins. All three intracellular loops as well as the carboxyl terminal tail of the receptor have been implicated. The GPCR is thought to interact with all three subunits of the G protein. As the receptor-G protein interaction can be disrupted by a number of treatments that block the carboxyl terminus, including pertussis toxin-catalyzed ADP-ribosylation of G_α and binding of monoclonal antibodies, the carboxy terminal region of the Gα subunit has been the most intensely investigated contact site. These studies have shown that the G_α. carboxy-terminal region is important not only to the interaction, but also plays a critical role in defining receptor specificity (Hamm et al., Science 241: 832-5 (1988); Osawa et al., J. Biol. Chem. 270: 31052-8 (1995); Garcia et al., EMBO 14: 4460-9 (1995); Sullivan et al., Nature 330: 758-760 (1987); Rasenick et al., J. Biol. Chem. 269: 21519-21525 (1994); West et al., J. Biol. Chem. 260: 14428-30 (1985); Conklin et al., 1993, Nature 363: 274-276; Conklin et al., Mol. Pharmacol. 50: 885-890 (1996)) **(35-42)**. Furthermore, it has been shown that peptides corresponding to the carboxy terminal region of a $G_{\alpha i}$ subunit can block GPCR

signaling events (Hamm et al., Science 241: 832-5 (1988); Gilchrist et al., J. Biol. Chem 273: 14912-19 (1998)) **(35, 43)**. However, prior to the present invention, it was unknown that G_i proteins were capable of functionally coupling to T1Rs and T2Rs.

[0053] Topologically, certain chemosensory GPCRs have an "N-terminal domain;" "extracellular domains;" "transmembrane domains" comprising seven transmembrane regions, and corresponding cytoplasmic, and extracellular loops; "cytoplasmic domains," and a "C-terminal domain" (see, e.g., Hoon *et al.*, *Cell*, 96:541-551 (1999) **(115)**; Buck & Axel, *Cell*, 65:175-187 (1991)) **(44)**. These domains can be structurally identified using methods known to those of skill in the art, such as sequence analysis programs that identify hydrophobic and hydrophilic domains (*see, e.g.*, Stryer, *Biochemistry*, (3rd ed. 1988) **(45)**; *see also* any of a number of Internet based sequence analysis programs. Such domains are useful for making chimeric proteins and for in vitro assays of the invention, *e.g.*, ligand binding assays.

[0054] "Extracellular domains" therefore refers to the domains of T1R and T2R polypeptides that protrude from the cellular membrane and are exposed to the extracellular face of the cell. Such domains generally include the "N terminal domain" that is exposed to the extracellular face of the cell, and optionally can include portions of the extracellular loops of the transmembrane domain that are exposed to the extracellular face of the cell, *i.e.*, the loops between transmembrane regions 2 and 3, between transmembrane regions 4 and 5, and between transmembrane regions 6 and 7.

[0055] The "N-terminal domain" region starts at the N-terminus and extends to a region close to the start of the first transmembrane domain. More particularly, in one embodiment of the invention, this domain starts at the N-terminus and ends approximately at the conserved glutamic acid at amino acid position 563 plus or minus approximately 20 amino acids. These extracellular domains are useful for *in* vitro ligand-binding assays, both soluble and solid phase. In addition, transmembrane regions, described below, can also bind ligand either in combination with the extracellular domain, and are therefore also useful for *in* vitro ligand-binding assays.

[0056] "Transmembrane domain," which comprises the seven "transmembrane regions," refers to the domain of T1R or T2R polypeptides that lies within the plasma membrane, and may also include the corresponding cytoplasmic (intracellular) and extracellular loops. In one embodiment, this region corresponds to the domain of T1R or T2R family members. In the case of T1R family member this starts approximately at the conserved glutamic acid residue at amino acid position 563 plus or minus 20 amino acids and ends approximately at the conserved tyrosine amino acid residue at position 812 plus or minus approximately 10 amino acids. The seven transmembrane regions and extracellular and cytoplasmic loops can be identified using standard methods, as described in Kyte & Doolittle, *J. Mol. Biol.*, 157:105-32 (1982)) **(46)**, or in Stryer, *supra* **(45)**.

[0057] "Cytoplasmic domains" refers to the domains of T1R or T2R polypeptides that face the inside of the cell, e.g., the "C-terminal domain" and the

intracellular loops of the transmembrane domain, e.g., the intracellular loop between transmembrane regions 1 and 2, the intracellular loop between transmembrane regions 3 and 4, and the intracellular loop between transmembrane regions 5 and 6. "C-terminal domain" refers to the region that spans the end of the last transmembrane domain and the 0-terminus of the protein, and which is normally located within the cytoplasm. In one embodiment, this region starts at the conserved tyrosine amino acid residue at position 812 plus or minus approximately 10 amino acids and continues to the C-terminus of the polypeptide.

[0058] The term "ligand-binding region" or "ligand-binding domain" refers to sequences derived from a taste receptor, particularly a taste receptor that substantially incorporates at least the extracellular domain of the receptor. In one embodiment, the extracellular domain of the ligand-binding region may include the N-terminal domain and, optionally, portions of the transmembrane domain, such as the extracellular loops of the transmembrane domain. The ligand-binding region may be capable of binding a ligand, and more particularly, a compound that enhances, mimics, blocks, and/or modulates taste, e.g., sweet, bitter, or umami taste. In the case of T2Rs, the compound bound by the ligand binding region will modulate bitter taste. In the case of T1Rs, the compound bound by the ligand-binding region will modulate sweet or umami taste.

[0059] The phrase "heteromultimer" or "heteromultimeric complex" in the context of the T1R receptors or polypeptides used in the assays of the present invention refers to a functional association of at least one T1R receptor and

another receptor, typically another T1R receptor polypeptide (or, alternatively another non-T1R receptor polypeptide). For clarity, the functional co-dependence of the T1Rs is described in this application as reflecting their possible function as heterodimeric taste receptor complexes. However, as discussed in Senomyx patent applications and publications which are incorporated by reference herein, **(10-12)** functional co-dependence may alternatively reflect an indirect interaction. For example, T1R3 may function solely to facilitate surface expression of T1R1 and T1R2, which may act independently as taste receptors. Alternatively, a functional taste receptor may be comprised solely of T1R3, which is differentially processed under the control of T1R1 or T1R2, analogous to RAMP-dependent processing of the calcium-related receptor. By contrast, in the case of T2Rs the eukaryotic cells used in the subject MAPK assays will preferably express a single T2R.

[0060] The phrase "modulator" or "modulatory compound" means any compound that itself affects the activity of a T1R or T2R or modulates (affects) the effect of another compound on T1R or T2R activity. Typically, modulation is determined by cell-based assays that detect the effect of a putative modulator or Gi signaling pathways, *e.g.*, assays that detect the effect of a compound on MAPK activity, cAMP levels or adenylyl cyclase activity.

[0061] The phrase "functional effects" in the context of assays for testing compounds that modulate at least one T1R or T2R family member mediated taste transduction includes the determination of any parameter that is indirectly or directly under the influence of the receptor, e.g., functional, physical and

chemical effects. It includes ligand binding, changes in ion flux, membrane potential, current flow, transcription, G protein binding, GPCR phosphorylation or dephosphorylation, conformation change-based assays, signal transduction, receptor-ligand interactions, second messenger concentrations (e.g., cAMP, cGMP, IP3, or intracellular Ca^{2+}), *in vitro, in vivo,* and *ex vivo* and also includes other physiologic effects such increases or decreases of neurotransmitter or hormone release. In the present invention, the assays will generally measure the effect of a compound on MAPK activation, cAMP accumulation or adenylyl cyclase activity in cell-based expression systems whereby the T1R or T2R is functionally coupled to a G_i protein such as $G_{\alpha i}$ and the assays are used to screen for putative sweeteners or sweet taste modulators or enhancers, umami taste modulators or enhancers, or bitter compounds or bitter taste modulators or enhancers, *e.g.*, bitter taste blockers. Such modulators have application for incorporation in foods, beverages, pharmaceuticals, and the like for human or animal consumption.

[0062] By "determining the functional effect" in the context of assays is meant assays for a compound that increases or decreases a parameter that is indirectly or directly under the influence of at least one T1R or T2R family member, *e.g.*, functional, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, *e.g.*, changes in spectroscopic characteristics (e.g., fluorescence, absorbency, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties, patch clamping, voltage-sensitive dyes, whole cell currents, radioisotope efflux,

inducible markers, oocyte T1R or T2R gene expression; tissue culture cell T1R or T2R expression; transcriptional activation of T1R or T2R genes; ligand-binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP, cGMP, and inositol triphosphate (IP3); changes in intracellular calcium levels; neurotransmitter release, conformational assays and the like. In the present invention, the effect of a putative modulator compound will be preferably assayed based on its effect on MAPK activation, cAMP accumulation, or adenylyl cyclase activity.

[0063] "Inhibitors," "activators," "enhancer," and "modulators" of T1R or T2R genes or proteins are used to refer to inhibitory, activating, or modulating molecules identified using *in vitro* and *in vivo* assays for taste transduction, e.g., ligands, agonists, antagonists, inversed agonists, and their homologues and mimetics. These compounds themselves modulate T1R or T2R activity or modulate the effect of another compound on T1R or T2R activity. In the present invention these molecules will preferably be identified using the subject cell-based MAPK or cAMP assays. In preferred embodiments, the "inhibitors" will block taste of a known bitter compound or enhance the taste of a known sweet or umami compound or compounds.

[0064] Inhibitors are compounds that, e.g., bind to, partially or totally block stimulation, decrease, prevent, delay activation, inactivate, desensitize, or down regulate taste transduction, e.g., antagonists. Activators are compounds that, *e.g.*, bind to, stimulate, increase, open, activate, facilitate, enhance activation, sensitize, or up regulate taste transduction, *e.g.*, agonists. Modulators include

compounds that, *e.g.*, alter the interaction of a receptor with: extracellular proteins that bind activators or inhibitor (*e.g.*, ebnerin and other members of the hydrophobic carrier family); G proteins; kinases (*e.g.*, homologues of rhodopsin kinase and beta adrenergic receptor kinases that are involved in deactivation and desensitization of a receptor); and arrestins, which also deactivate and desensitize receptors. Modulators can include genetically modified versions of T1R or T2R family members, *e.g.*, with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, small chemical molecules and the like. Such assays for inhibitors and activators include, *e.g.*, expressing T1R or T2R family members in cells or cell membranes, applying putative modulator compounds, in the presence or absence of tastants, *e.g.*, sweet, umami or bitter tastants, and then determining the functional effects on taste transduction, as described above. Samples or assays comprising T1R or T2R family members that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of modulation. Positive control samples (*e.g.* a sweet, umami, or bitter tastant without added modulators) are assigned a relative T1R or T2R activity value of 100%.

[0065] Negative control samples (*e.g.*, buffer without an added taste stimulus) are assigned a relative T1R or T2R activity value of 0%. Inhibition of a T1R or T2R is achieved when a mixture of the positive control sample and a modulator result in the T1R or T2R activity value relative to the positive control is about 80%, optionally 50% or 25-0%. Activation of a T1R or T2R by a modulator alone

is achieved when the T1R activity value relative to the positive control sample is 10%, 25%, 50%, 75%, optionally 100%, optionally 150%, optionally 200-500%, or 1000-3000% higher.

[0066] The terms "purified," "substantially purified," and "isolated" as used herein refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated," when referring to a nucleic acid or protein, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human body. Any degree of purification or concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

[0067] The term "nucleic acid" or "nucleic acid sequence" refers to a deoxyribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded form. The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like structures with synthetic backbones (*see e.g.*, *Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Antisense* Strategies, *Annals of* the N. Y. Academy *of* Sciences, Vol. 600, Eds. Baserga et al. (NYAS 1992); Milligan J. *Med. Chem.* 36:1923-1937 (1993); *Antisense Research and Applications* (1993, CRC Press), Mata, *Toxicol. Appl. Pharmacol.* 144:189-197 (1997); Strauss-Soukup, *Biochemistry* 36:8692-8698 (1997); Samstag, *Antisense Nucleic Acid Drug Dev*, 6:153-156 (1996)) **(47-53)**.

[0068] Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating, *e.g.*, sequences in which the third position of one or more selected codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al, Nucleic* Acid Res., 19:5081 (1991); Ohtsuka *et al.*, J. Biol. Chem., 260:2605-2608 (1985); Rossolini et *al., Mol. Cell. Probes*, 8:91-98 (1994)) **(54-56)**. The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

[0069] The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms

apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

[0070] The term "plasma membrane translocation domain" or simply "translocation domain" means a polypeptide domain that, when incorporated into a polypeptide coding sequence, can with greater efficiency "chaperone" or "translocate" the hybrid ("fusion") protein to the cell plasma membrane than without the domain. For instance, a "translocation domain" may be derived from the amino terminus of the bovine rhodopsin receptor polypeptide, a 7-transmembrane receptor. However, rhodopsin from any mammal may be used, as can other translocation facilitating sequences. Thus, the translocation domain is particularly efficient in translocating 7-transmembrane fusion proteins to the plasma membrane, and a protein (*e.g.*, a taste receptor polypeptide) comprising an amino terminal translocating domain will be transported to the plasma membrane more efficiently than without the domain. However, if the N-terminal domain of the polypeptide is active in binding, as with the T1R or T2R receptors of the present invention, the use of other translocation domains may be preferred. For instance, a PDZ domain-interacting peptide, as described herein, may be used.

[0071] The "translocation domain," "ligand-binding domain", and chimeric receptors compositions described herein also include "analogs," or "conservative variants" and "mimetics" ("peptidomimetics") with structures and activity that

substantially correspond to the exemplary sequences. Thus, the terms "conservative variant" or "analog" or "mimetic" refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the polypeptide's (the conservative variant's) structure and/or activity, as defined herein. These include conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (*e.g.*, acidic, basic, positively or negatively charged, polar or non-polar, etc.) such that the substitutions of even critical amino acids does not substantially alter structure and/or activity.

[0072] More particularly, "conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences . Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein.

[0073] For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide.

[0074] Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein, which encodes a polypeptide, also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid, which encodes a polypeptide, is implicit in each described sequence.

[0075] Conservative substitution tables providing functionally similar amino acids are well known in the art. For example, one exemplary guideline to select conservative substitutions includes (original residue followed by exemplary substitution): ala/gly or ser; arg/lys; asn/gln or his; asp/glu; cys/ser; gln/asn; gly/asp; gly/ala or pro; his/asn or gin; ile/leu or val; leu/ile or val; lys/arg or gln or glu; met/leu or tyr or lie; phe/met or leu or tyr; ser/thr; thr/ser; trp/tyr; tyr/trp or phe; val/ile or leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g.*, Creighton, *Proteins*, W.H. Freeman and Company (1984); Schultz and Schimer, *Principles of Protein Structure*, Springer-Verlag (1979)) **(57-58)**. One of skill in the art will appreciate that the above-identified substitutions are not the only possible conservative

substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

[0076] The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, *e.g.*, translocation domains, ligand-binding domains, or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or may be a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity.

[0077] As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the invention, *i.e.*, that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, i.e., to induce

or stabilize a secondary structure, *e.g.*, a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, *e.g.*, glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, *e.g.*, ketomethylene (*e.g.*, - C(=O)-CH_2- for -C(=O)-NH-), aminomethylene (CH2-NH), ethylene, olefin (CH=CH), ether (CH_2-O), thioether (CH2-S), tetrazole (CN_4), thiazole, retroamide, thioamide, or ester (see, e.g., Spatola, *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins,* Vol. 7, pp 267-357, "Peptide Backbone Modifications," Marcell Dekker, NY (1983)) **(157)**. A polypeptide can also be characterized as a mimetic by containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

[0078] A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include ^{32}P, fluorescent dyes, electron-dense reagents, enzymes (*e.g.*, as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, *e.g.*, by incorporating a radiolabel

into the peptide or used to detect antibodies specifically reactive with the peptide.

[0079] A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.

[0080] As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.*, A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are optionally directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

[0081] The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, *e.g.*, a promoter from one source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

[0082] A "promoter" is defined as an array of nucleic acid sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions.

[0083] An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

[0084] As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (*e.g.*, "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, *e.g.*, inducible or constitutive expression of a fusion protein comprising a translocation domain of the invention and a nucleic acid sequence amplified using a primer of the invention.

[0085] As used herein, a "stable cell line" refers to a cell line, which stably, *i.e.* over a prolonged period, expresses a heterologous nucleic sequence, *i.e.,* a T1R, T2R or G protein. In preferred embodiments, such stable cell lines will be produced by transfecting appropriate cells, typically mammalian cells, e.g. HEK-293 cells, with a linearized vector that contains a T1R or T2R expression construct that expresses at least one T1R or T2R, *i.e.*, T1R1, T1R2 and/or T1R3 or a T2R. Most preferably, such stable cell lines that express a functional T1R or T2R receptor will be produced by co-transfecting two linearized plasmids that express hT1R1 and hT1R3 or hT1R2 and hT1R3 or a single line plasmid that expresses a specific T2R and an appropriate selection procedure to generate cell lines having these genes stably integrated therein. Most preferably, the cell line will also stably express a G protein preferably a G_i such as $G_{\alpha i}$ or $G_{\alpha 15}$.

[0086] "Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragment thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively.

[0087] An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kDa) and one "heavy" chain (about 50-70 kDa). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms "variable light chain" (VL) and "variable heavy chain" (VH) refer to these light and heavy chains respectively.

[0088] A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.*, an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

[0089] An "anti-T1R" antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by a T1R gene, cDNA, or a subsequence or variant thereof.

[0090] An "anti-T2R" antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by T2R gene, cDNA, or a subsequence or variant thereof.

[0091] An "anti-activated MAPK antibody" or an "anti-phospho MAPK antibody" refers to an antibody or antibody fragment that specifically binds to an activated (phosphorylated) form of MAPK.

[0092] A "ligand that detects cAMP" is any moiety that specifically detects cAMP levels.

[0093] The term "immunoassay" is an assay that uses an antibody to specifically bind an antigen. The immunoassay is characterized by the use of specific binding properties of a particular antibody to isolate, target, and/or quantify the antigen. In a preferred embodiment of the invention, MAPK activity or cAMP levels will be immunoassayed in eukaryotic cells using an antibody that specifically recognizes an activated form of MAPK or cAMP.

[0094] The phrase "specifically (or selectively) binds" to an antibody or, "specifically (or selectively) immunoreactive with," when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein in a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a

particular protein at least two times the background and do not substantially bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. For example, polyclonal antibodies raised to a T1R or T2R family member from specific species such as rat, mouse, or human can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with the T1R or T2R polypeptide or an immunogenic portion thereof and not with other proteins, except for orthologs or polymorphic variants and alleles of the T1R or T2R polypeptide. This selection may be achieved by subtracting out antibodies that cross-react with T1R or T2R molecules from other species or other T1R or T2R molecules. Antibodies can also be selected that recognize only T1R GPCR family members but not GPCRs from other families. In the case of antibodies to activated MAPKs, suitable polyclonal and monoclonal antibodies are commercially available.

[0095] A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein *(see, e.g.,* Harlow & Lane, *Antibodies, A Laboratory Manual, (1988)* **(59)**, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity). Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 to 100 times background.

[0096] The phrase "selectively associates with" refers to the ability of a nucleic acid to "selectively hybridize" with another as defined above, or the ability of an antibody to "selectively (or specifically) bind to a protein, as defined above.

[0097] The term "expression vector" refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, *i.e.*, drive only transient expression in a cell. The term includes recombinant expression "cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

[0098] By "host cell" is meant a cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, worm or mammalian cells such as CHO, Hela, BHK, HEK-293, and the like, e.g., cultured cells, explants, and cells *in vivo*.

[0099] The terms "a," "an," and "the" are used in accordance with long-standing convention to refer to one or more.

[00100] The term "about", as used herein when referring to a measurable value such as a percentage of sequence identity (e.g., when comparing nucleotide and amino acid sequences as described herein below), a nucleotide or protein length,

an amount of binding, etc. is meant to encompass variations of ±20% or ±10%, more preferably ±5%, even more preferably ±1, and still more preferably ±.1% from the specified amount, as such variations are appropriate to perform a disclosed method or otherwise carry out the present invention.

[00101] The term "substantially identical", is used herein to describe a degree of similarity between nucleotide sequences, and refers to two or more sequences that have at least about least 60%, preferably at least about 70%, more preferably at least about 80%, more preferably about 90% to 99%, still more preferably about 95% to about 99%, and most preferably about 99% nucleotide identify, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms or by visual inspection. Preferably, the substantial identity exists in nucleotide sequences of at least about 100 residues, more preferably in nucleotide sequences of at least about 150 residues, and most preferably in nucleotide sequences comprising a full length coding sequence. The term "full length" is used herein to refer to a complete open reading frame encoding a functional T1R or T2R polypeptide, as described further herein below. Methods for determining percent identity between two polypeptides are defined herein below under the heading "Nucleotide and Amino Acid Sequence Comparisons".

[00102] In one aspect, substantially identical sequences can be polymorphic sequences. The term "polymorphic" refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. An allelic difference can be as small as one base pair.

[00103] In another aspect, substantially identical sequences can comprise mutagenized sequences, including sequences comprising silent mutations. A mutation can comprise one or more residue changes, a deletion of residues, or an insertion of additional residues.

[00104] Another indication that two nucleotide sequences are substantially identical is that the two molecules hybridize specifically to or hybridize substantially to each other under stringent conditions. In the context of nucleic acid hybridization, two nucleic acid sequences being compared can be designated a "probe" and a "target." A "probe" is a reference nucleic acid molecule, and a "target" is a test nucleic acid molecule, often found within a heterogeneous population of nucleic acid molecules. A "target sequence" is synonymous with a "test sequence."

[00105] A preferred nucleotide sequence employed for hybridization studies or assays includes probe sequences that are complementary to or mimic at least an about 14 to 40 nucleotide sequence of a nucleic acid molecule of the present invention. Preferably, probes comprise 14 to 20 nucleotides, or even longer where desired, such as 30, 40, 50, 60, 100, 200, 300, or 500 nucleotides or up to the full length of the particular T1R or T2R. Such fragments can be readily prepared by, for example, chemical synthesis of the fragment, by application of nucleic acid amplification technology, or by introducing selected sequences into recombinant vectors for recombinant production.

[00106] The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex nucleic acid mixture (*e.g.*, total cellular DNA or RNA).

[00107] The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (*e.g.*, total cellular or library DNA or RNA).

[00108] The phrase "stringent hybridization conditions" and "stringent hybridization wash conditions" refer to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is that in Tigssen, *Techniques in Biochemistry and Molecular Biology – Hybridization With Nucleic Probes,* "Overview of principles of hybridization and the strategy of nucleic acid assays." (1973) Generally, highly stringent hybridization and wash conditions are selected to be about 5-10°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength pH. The Tm is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at Tm, 50% of the probes are occupied at equilibrium).

[00109] Stringent conditions will be those in which the salt concentration is less than about 1.0M sodium ion, typically about 0.01 to 1.0M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (*e.g.*, 10 to 50 nucleotides) and at least about 60°C for long probes (*e.g.*, greater than 50 nucleotides). Stringent conditions may also be achieved with the additional of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, optionally 10 times background hybridization. Exemplary stringent hybridization conditions are:

[00110] 50% formamide, 5X SSC, and 1% SDS, incubating at 42°C or 5X SSC, 1% SDS, incubating at 65°C. The hybridization and wash steps effected in said exemplary stringent hybridization conditions are each effected for at least 1, 2, 5, 10, 15, 30, 60, or more minutes. Preferably, the wash and hybridization steps are each effected for at least 5 minutes, and more preferably, 10 minutes, 15 minutes, or more than 15 minutes.

[00111] The phrase "hybridizing substantially to" refers to complementary hybridization between a probe nucleic acid molecule and a target nucleic acid molecule and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired hybridization.

[00112] An example of stringent hybridization conditions for Southern or Northern Blot analysis of complementary nucleic acids having more than about

100 complementary residues is overnight hybridization in 50% formamide with 1 mg of heparin at 42°C. An example of highly stringent wash conditions is 15 minutes in 0.1X SSC at 65°C. An example of stringent wash conditions is 15 minutes in 0.2X SSC buffer at 65°C. See Sambrook et al., eds (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York **(60)** for a description of SSC buffer. Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example of medium stringency wash conditions for a duplex of more than about 100 nucleotides, is 15 minutes in 1X SSC at 45°C. An example of low stringency wash for a duplex of more than about 100 nucleotides, is 15 minutes in 4X to 6X SSC at 40°C. For short probes (*e.g.*, about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1 M Na^+ ion, typically about 0.01 to 1 M Na^+ ion concentration (or other salts) at pH 7.0-8.3, and the temperature is typically at least about 30°C. Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2-fold (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization.

[00113] The following are additional examples of hybridization and wash conditions that can be used to identify nucleotide sequences that are substantially identical to reference nucleotide sequences of the present invention: a probe nucleotide sequence preferably hybridizes to a target nucleotide sequence in 7% sodium dodecyl sulphate (SDS), 0.5M $NaP0_4$, 1 mM

EDTA at 50°C followed by washing in 2X SSC, 0.1% SDS at 50°C; more preferably, a probe and target sequence hybridize in 7% sodium dodecyl sulphate (SDS), 0.5M $NaP0_4$, 1 mM EDTA at 50°C followed by washing in 1X SSC, 0.1% SDS at 50°C; more preferably, a probe and target sequence hybridize in 7% sodium dodecyl sulphate (SDS), 0.5M NaP04, 1 MM EDTA at 50°C followed by washing in 0.5X SSC, 0.1% SDS at 50°C; more preferably, a probe and target sequence hybridize in 7% sodium dodecyl sulphate (SIDS), 0.5M $NaP0_4$, 1mM EDTA at 50°C followed by washing in 0.1X SSC, 0.1 SDS at 50°C; more preferably, a probe and target sequence hybridize in 7% sodium dodecyl sulphate (SDS), 0.5M $NaP0_4$, 1mM EDTA at 50°C followed by washing in 0.1 X SSC, 0.1 % SDS at 65°C.

[00114] A further indication that two nucleic acid sequences are substantially identical is that proteins encoded by the nucleic acids are substantially identical, share an overall three-dimensional structure, or are biologically functional equivalents. Nucleic acid molecules that do not hybridize to each other under stringent conditions are still substantially identical if the corresponding proteins are substantially identical. This can occur, for example, when two nucleotide sequences comprise conservatively substituted variants as permitted by the genetic code.

[00115] Nucleic acids that do not hybridize to each other under stringent conditions are still substantially related if the polypeptides that they encode are substantially related. This occurs, for example, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In

such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1X SSC at 45°C. Such hybridizations and wash steps can be carried out for, *e.g.*, 1, 2, 5, 10, 15, 30, 60, or more minutes. Preferably, the wash and hybridization steps are each effected for at least 5 minutes. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.

[00116] The term "conservatively substituted variants" refers to nucleic acid sequences having degenerate codon substitutions wherein the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues. See Batzer et al. (1991) *Nucleic Acids Res* 19:5081; Ohtsuka et al. (1985) *J Biol Chem* 260:2605-2608; and Rossolini et al. (1994) *Mol Cell Probes* 8:91-98 **(54-56)**.

[00117] The term T1R or T2R also encompasses nucleic acids comprising subsequences and elongated sequences of a T1R or T2R nucleic acid, including nucleic acids complementary to a T1R or T2R nucleic acid, T1R or T2R RNA molecules, and nucleic acids complementary to T1R or T2R RNAs (cRNAs).

[00118] The term "subsequence" refers to a sequence of nucleic acids that comprises a part of a longer nucleic acid sequence. An exemplary subsequence is a probe, described herein above, or a primer. The term "primer" as used herein

refers to a contiguous sequence comprising about 8 or more deoxyribonucleotides or ribonucleotides, preferably 10-20 nucleotides, and more preferably 20-30 nucleotides of a selected nucleic acid molecule. The primers of the invention encompass oligonucleotides of sufficient length and appropriate sequence so as to provide initiation of polymerization on a nucleic acid molecule of the present invention.

[00119] The term "elongated sequence" refers to an addition of nucleotides (or other analogous molecules) incorporated into the nucleic acid. For example, a polymerase (e.g., a DNA polymerase) can add sequences at the 3' terminus of the nucleic acid molecule. In addition, the nucleotide sequence can be combined with other DNA sequences, such as promoters, promoter regions, enhancers, polyadenylation signals, intronic sequences, additional restriction enzyme sites, multiple cloning sites, and other coding segments.

[00120] The term "complementary sequences," as used herein, indicates two nucleotide sequences that comprise antiparallel nucleotide sequences capable of pairing with one another upon formation of hydrogen bonds between base pairs. As used herein, the term "complementary sequences" means nucleotide sequences which are substantially complementary, as can be assessed by the same nucleotide comparison methods set forth below, or is defined as being capable of hybridizing to the nucleic acid segment in question under relatively stringent conditions such as those described herein. A particular example of a complementary nucleic acid segment is an antisense oligonucleotide.

[00121] The term "gene" refers broadly to any segment of DNA associated with a biological function. A gene encompasses sequences including but not limited to a coding sequence, a promoter region, a cis-regulatory sequence, a non-expressed DNA segment that is a specific recognition sequence for regulatory proteins, a non-expressed DNA segment that contributes to gene expression, a DNA segment designed to have desired parameters, or combinations thereof. A gene can be obtained by a variety of methods, including cloning from a biological sample, synthesis based on known or predicted sequence information, and recombinant derivation of an existing sequence.

[00122] The term "chimeric gene," as used herein, refers to a promoter region operatively linked to a T1R or T2R sequence, including a T1R or T2R cDNA, a T1R or T2R nucleic acid encoding an antisense RNA molecule, a T1R or T2R nucleic acid encoding an RNA molecule having tertiary structure (*e.g.*, a hairpin structure) or a T1R or T2R nucleic acid encoding a double-stranded RNA molecule. The term "chimeric gene" also refers to a T1R or T2R promoter region operatively linked to a heterologous sequence.

[00123] The term "operatively linked", as used herein, refers to a functional combination between a promoter region and a nucleotide sequence such that the transcription of the nucleotide sequence is controlled and regulated by the promoter region. Techniques for operatively linking a promoter region to a nucleotide sequence are known in the art.

[00124] The term "vector" is used herein to refer to a nucleic acid molecule having nucleotide sequences that enable its replication in a host cell. A vector can also include nucleotide sequences to permit ligation of nucleotide sequences within the vector, wherein such nucleotide sequences are also replicated in a host cell. Representative vectors include plasmids, cosmids, and viral vectors. A vector can also mediate recombinant production of a T1R or T2R polypeptide, as described further herein below.

[00125] The term "construct", as used herein to describe a type of construct comprising an expression construct, refers to a vector further comprising a nucleotide sequence operatively inserted with the vector, such that the nucleotide sequence is recombinantly expressed.

[00126] The terms "recombinantly expressed" or "recombinantly produced" are used interchangeably to refer generally to the process by which a polypeptide encoded by a recombinant nucleic acid is produced.

[00127] The term "heterologous nucleic acids" refers to a sequence that originates from a source foreign to an intended host cell or, if from the same source, is modified from its original form. Thus, preferably recombinant T1R or T2R nucleic acids comprise heterologous nucleic acids. A heterologous nucleic acid in a host cell can comprise a nucleic acid that is endogenous to the particular host cell but has been modified, for example by mutagenesis or by isolation from native cis-regulatory sequences. A heterologous nucleic acid also includes non-naturally occurring multiple copies of a native nucleotide sequence.

A heterologous nucleic acid can also comprise a nucleic acid that is incorporated into a host cell's nucleic acids at a position wherein such nucleic acids are not ordinarily found.

[00128] Nucleic acids used in the cell-based assays of the present invention preferably MAPK and cAMP assays can be cloned, synthesized, altered, mutagenized, or combinations thereof. Standard recombinant DNA and molecular cloning techniques used to isolate nucleic acids are known in the art. Site-specific mutagenesis to create base pair changes, deletions, or small insertions are also known in the art. *See e.g.*, Sambrook et al. (eds.) *Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press*, Cold Spring Harbor, New York (1989); Silhavy et al. *Experiments with Gene Fusions.* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1984); Glover & Hames *DNA Cloning: A Practical Approach*, 2nd ed. IRL Press and Oxford University Press, Oxford/New York (1995); Ausubel (ed.) *Short Protocols in Molecular Biology*, 3rd ed. Wiley, New York (1995) **(60-63)**.

[00129] The term "substantially identical", as used herein to describe a level of similarity between a particular T1R or T2R protein and a protein substantially identical to the T1R or T2R protein, refers to a sequence that is at least about 35% identical to the particular T1R or T2R protein, when compared over the full length of the T1R or T2R protein. Preferably, a protein substantially identical to the T1R or T2R protein used in the present invention comprises an amino acid sequence that is at least about 35% to about 45% identical to a particular T1R or T2R, more preferably at least about 45% to about 55% identical thereto, even

more preferably at least about 55% to about 65% identical thereto, still more preferably at least about 65% to about 75% identical thereto, still more preferably at least about 75% to about 85% identical thereto, still more preferably at least about 85% to about 95% identical thereto, and still more preferably at least about 95% to about 99% identical thereto when compared over the full length of the particular T1R or T2R. The term "full length" refers to a functional T1R or T2R polypeptide. Methods for determining percent identity between two polypeptides are also defined herein below under the heading "Nucleotide and Amino Acid Sequence Comparisons".

[00130] The term "substantially identical," when used to describe polypeptides, also encompasses two or more polypeptides sharing a conserved three-dimensional structure. Computational methods can be used to compare structural representations, and structural models can be generated and easily tuned to identify similarities around important active sites or ligand binding sites. See Saqi et al. *Bioinformatics* 15:521-522 (1999); Barton *Acta Crystallogr D Biol Crystallogr* 54:1139-1146 (1998); Henikoff et al. *Electrophoresis* 21:1700-1706 (2000); and Huang et al. *Pac Symp Biocomput*:230-241 (2000) **(64-67)**.

[00131] Substantially identical proteins also include proteins comprising amino acids that are functionally equivalent to a T1R or T2R according to the invention. The term "functionally equivalent" in the context of amino acids is known in the art and is based on the relative similarity of the amino acid side-chain substituents. *See* Henikoff & Henikoff *Adv Protein Chem* 54:73-97 (2000) **(68)**. Relevant factors for consideration include side-chain hydrophobicity,

hydrophilicity, charge, and size. For example, arginine, lysine, and histidine are all positively charged residues; that alanine, glycine, and serine are all of similar size; and that phenylalanine, tryptophan, and tyrosine all have a generally similar shape. By this analysis, described further herein below, arginine, lysine, and histidine; alanine, glycine, and serine; and phenylalanine, tryptophan, and tyrosine; are defined herein as biologically functional equivalents.

[00132] In making biologically functional equivalent amino acid substitutions, the hydropathic index of amino acids can be considered. Each amino acid has been assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics, these are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

[00133] The importance of the hydropathic amino acid index in conferring interactive biological function on a protein is generally understood in the art (Kyte et al., *J. Mol. Biol.* 157(1):105-32 (1982)) **(69)**. It is known that certain amino acids can be substituted for other amino acids having a similar hydropathic index or score and still retain a similar biological activity. In making changes based upon the hydropathic index, the substitution of amino acids whose hydropathic indices are within ±2 of the original value is preferred, those which are within ±1 of the original value are particularly preferred, and those within ±0.5 of the original value are even more particularly preferred.

[00134] It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Patent No. 4,554,101 describes that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigenicity, e.g., with a biological property of the protein. It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent protein.

[00135] As detailed in U.S. Patent No. 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+ 3.0); lysine (+ 3.0); aspartate (+ 3.0±1); glutamate (+ 3.0±1); serine (+ 0.3); asparagine (+ 0.2); glutamine (+ 0.2); glycine (0); threonine (-0.4); proline (-0.5±1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4).

[00136] In making changes based upon similar hydrophilicity values, the substitution of amino acids whose hydrophilicity values are within ±2 of the original value is preferred, those which are within ±1 of the original value are particularly preferred, and those within ±0.5 of the original value are even more particularly preferred.

[00137] The term "substantially identical" also encompasses polypeptides that are biologically functional equivalents of a particular T1R or T2R polypeptide. The term "functional" includes an activity of an T1R or T2R polypeptide, for example activating intracellular signaling pathways (e.g., coupling with

gustducin) and mediating taste perception. Preferably, such activation shows a magnitude and kinetics that are substantially similar to that of a cognate T1R or T2R polypeptide in vivo. Representative methods for assessing T1R or T2R activity are described in the patent applications incorporated by reference herein.

[00138] The assays of the present invention also can use functional fragments of a particular T1R or T2R polypeptide. Such functional portion need not comprise all or substantially all of the amino acid sequence of a native T1R or T2R gene product. The assays of the present invention also can use functional polypeptide sequences that are longer sequences than that of a native T1R or T2R polypeptide. For example, one or more amino acids can be added to the N-terminus or C-terminus of a T1R or T2R polypeptide. Such additional amino acids can be employed in a variety of applications, including but not limited to purification applications. Methods of preparing elongated proteins are known in the art.

[00139] "MAPK" or "MAP Kinase" refers to a mitogen activated protein kinase, the expression of which is activated by some functional GPCRs, i.e., T2Rs and T1Rs.

[00140] "MAPK" or "MAP Kinase" activation specific ligands" refers to a ligand, preferably a polyclonal or monoclonal antibody or fragment thereof that specifically binds an activated form of MAPK, e.g., p42/p44 MAPK or p38/MAPK. Antibodies that specifically bind the activated (phosphorylated) form of MAPK

are commercially available and include the phosph-p44/p42 MAP Kinase antibody #9106 available from Cell Signaling Technologies, the polyclonal anti-phospho-p44/42 MAPK and anti-phospho-p38 MAPK antibodies available from UBI, (Lake Placid, NY, USA) and New England Biolabs (Beverly, MA, USA), the anti-phospho-p44/42 MAPK antibodies reported by Discovery Research Laboratories III, Takeda Chemical Indust. Ltd., (Oskaka Japan) (Tan et al., J. Immunol. Meth. 232(1-2): 87-97 (1998)) **(70)**.

[00141] "Ligand" or "compound" that "activates MAPK" refers to a compound which when contacted with a eukaryotic cell that expresses a functional GPCR, herein at least one functional T1R or T2R, results in a detectable increase in the activated form of MAPK. This increase will preferably will be detected by antibody-based detection methods that use an antibody that specifically binds to an activated form of MAPK.

[00142] "PLC" refers to phospholipase C. In the present invention, "a ligand or compound that activates MAPK" may activate MAPK in cells via a pathway that is independent of PLC activation.

Cell Based Assays of the Present Invention

[00143] This, in one aspect, present invention generally relates to cell-based assays for identifying compounds that modulate the activity of at least one T1R or T2R taste receptor, wherein the assays comprise contacting a eukaryotic cell that stably or transiently expresses at least one functional T1R or T2R and a G protein that functionally couples therewith, *e.g.* a G_i protein such as $G\alpha_i$ with a putative modulator of said functional T1R or T2R, and assaying the effect of said

putative agonist or antagonist compound on G_i mediated signaling pathways, *e.g.,* by assaying the effect of said putative modulation on MAPK activation, cAMP accumulation or adenylyl cyclase activity. For example, a modulator compound will result, *e.g.,* in a detectable increase or decrease in the amount of an activated form of MAPK, i.e., phosphorylated MAPK, e.g., phosphorylated p44/42 MAP Kinase or phosphorylated p38 MAP Kinase, and will elicit this effect on MAPK activation by a pathway independent of PLC activation or will result in detectable increase or decrease in cAMP accumulation, or will result in a change (*e.g.,* decrease) in adenylyl cyclase activity. However, the invention embraces any cell-based assays that identify compounds that modulate to a TRGPCR (T1R or T2R)/$G_{\alpha i}$ mediated signaling pathway.

[00144] The eukaryotic cells used in the subject assays, preferably MAPK, cAMP or adenylyl cyclase assays, will stably or transiently express at least one functional T1R or T2R. Preferably, the eukaryotic cell will either stably or transiently express a functional T1R1/T1R3 umami taste receptor or a functional T1R2/T1R3 sweet taste receptor or will stably or transiently express a desired functional T2R, preferably a functional human T1R or T2R taste receptor. In order to produce a functional taste receptor, the eukaryotic cell will further be transfected to stably or transiently express or will endogenously express a G protein that couples with said T1R(s) or T2R thereby resulting in a functional taste receptor. Examples of suitable G proteins are known in the art and are referred in the patent applications incorporated by reference herein. In a preferred embodiment, the G protein will comprise a Gi protein selected from

$G\alpha_i$, i.e. $G\alpha_{i1-1}$, $G\alpha_{i1-2}$, $G\alpha_{i1-3}$, $G\alpha_{i0-1}$, and $G\alpha_{i0-2}$. Alternatively, the G protein will comprise $G\alpha_{15}$, α-transcucin, gustducin, $G_{\alpha z}$ or a functional chimera or variant thereof that couples with the T1R(s) or T2R expressed by the eukaryotic cell.

[00145] The present assays can be effected. using any eukaryotic cell that functionally expresses the particular T1R(s) or T2R, and which cell, when contacted with an activator of said T1R or T1R results in an increase in an activated form of MAPK, or a decrease in cAMP accumulation or a reduction in adenylyl cyclase activity by a pathway that is independent of PLC activation. Examples of suitable eukaryotic cells include amphibian, yeast, insect, amphibian, worm and mammalian cells. Specific examples of suitable cells for use in the subject cell-based assays include HEK293 cells, BHK cells, CHO cells, Hela cells and Xenopus oocytes,.

[00146] In a preferred embodiment the eukaryotic cells used in the subject cell-based assays, *e.g.*, MAPK, cAMP and adenylyl cyclase assays will comprise HEK293 cells that stably or transiently express at least one or functional T1R or T2R taste receptor by the transfection of such cells with a cDNA or cDNAs encoding said at least one T1R or T2R. For example, HEK293 cells stably expressing the large T cell antigen and the promiscuous G protein $G\alpha_{15}$ (HEK293T-$G\alpha_{15}$) or $G_{\alpha i}$ can be transiently transfected with a particular taste receptor plasmid by known transfection methods, e.g., by use of Ca^{2+} phosphate or lipid-based systems, or other transformation methods referenced supra. As noted previously, the T1R or T2R expressing cell will further express

endogenously or be engineered to express a G protein that functionally couples therewith, *e.g.*, a G protein selected from the $G_{\alpha i}$ proteins identified previously.

[00147] Cells that stably or transiently express the particular taste receptor are used in assays that measure the effect of at least one putative T1R or T2R modulatory compound on $G_{\alpha i}$–mediated signaling pathways, *e.g.*, by measuring its effect on MAPK activation, cAMP accumulation or adenylyl cyclase activity. The MAPK or cAMP assays of the present invention can use immobilized cells or cells in suspension. In a preferred embodiment the taste receptor expressing cells will be seeded into multi-well culture plates, e.g., 6-well culture plates. However, other in vitro cell culture devices can be substituted therefore, and is not critical to the invention.

[00148] In a typical MAPK or cAMP assay according to the invention, functional expression of the T1R or T2R expressing eukaryotic cell is allowed to proceed for a certain time, e.g., on the order of about 48 hours, and then taste receptor expressing cells are stimulated with a putative modulatory compound for a fixed time, e.g., about 5 minutes, and then the reaction is then stopped, e.g., by the addition of ice-cold buffer, and the cells are then assayed for changes in activated MAPK, cAMP or adenylyl cyclase activity. However, these reaction times may be shortened or lengthened within wide limits.

[00149] The level of activated MAPK produced by such cells is detected in whole cells or cell lysates. In a preferred embodiment, cell lysates are prepared by known methods, and detected by activated cAMP, MAPK or adenylyl cyclase

activity is detected by known methods. For example, activated MAPK can be the use of a polyclonal or monoclonal antibody or fragment thereof that specifically recognizes an activated (phosphorylated) form of MAPK. In a preferred embodiment, activation of MAPK is detected by Western analysis of cell lysates using a specific monoclonal antibody that recognizes phosphorylated (active) MAPK (Phospho-p44/42 MAP Kinase antibody #9106 available from Cell Signaling Technologies) or another commercially available antibody that specifically recognizes activated MAPK.

Exemplification of Cell-Based Assays According to the Invention

[00150] The following are exemplary of cell-based assays that may be used according to the invention for detecting the effect of a putative modulator on T1R or T2R activity.

1. GTP Assay

[00151] For GPCRs T1R OR T2R, a measure of receptor activity is the binding of GTP by cell membranes containing receptors. In the method described by Traynor and Nahorski, 1995, Mol. Pharmacol. 47: 848-854, (1995) **(130)** one essentially measures G-protein coupling to membranes by detecting the binding of labelled GTP. For GTP binding assays, membranes isolated from cells expressing the receptor are incubated in a buffer containing 20 mM HEPES, pH 7.4, 100 mM NaCl, and 10 mM $MgCl_2$, 80 pM ..^{35}S-GTPγS and 3μM GDP.

[00152] The assay mixture is incubated for 60 minutes at 30°C., after which unbound labelled GTP is removed by filtration onto GF/B filters. Bound, labelled

GTP is measured by liquid scintillation counting. The presence and absence of a candidate modulator of T1R or T2R activity. A decrease of 10% or more in labelled GTP binding as measured by scintillation counting in an assay of this kind containing a candidate modulator, relative to an assay without the modulator, indicates that the candidate modulator inhibits T1R or T2R activity. A compound is considered an agonist if it induces at least 50% of the level of GTP binding when the compound is present at 1μM or less.

[00153] GTPase activity is measured by incubating the membranes containing a T1R or T2R polypeptide with .γ^{32}P-GTP. Active GTPase will release the label as inorganic phosphate, which is detected by separation of free inorganic phosphate in a 5% suspension of activated charcoal in 20 mM H_3PO_4, followed by scintillation counting. Controls include assays using membranes isolated from cells not expressing T1R or T2R (mock-transfected), in order to exclude possible non-specific effects of the candidate compound.

[00154] [0158] In order to assay for the effect of a candidate modulator on T1R or T2R-regulated GTPase activity, membrane samples are incubated with and without the modulator, followed by the GTPase assay. A change (increase or decrease) of 10% or more in the level of GTP binding or GTPase activity relative to samples without modulator is indicative of T1R or T2R modulation by a candidate modulator.

[00155] 2. **<u>Downstream Pathway Activation Assays</u>:**

[00156] i) .Calcium Flux--The Aequorin-based Assay:

[00157] The aequorin assay takes advantage of the responsiveness of mitochondrial apoaequorin to intracellular calcium release induced by the activation of GPCRs (Stables et al., Anal. Biochem. 252:115-126 (1997); Detheux et al., 2000, J. Exp. Med., 192 1501-1508 (2000) **(131-132)**; both of which are incorporated herein by reference). Briefly, T1R or T2R-expressing clones are transfected to coexpress mitochondrial apoaequorin and $G_{\alpha 16}$. Cells are incubated with 5μM Coelenterazine H (Molecular Probes) for 4 hours at room temperature, washed in DMEM-F12 culture medium and resuspended at a concentration of 0.5.times.10.sup.6 cells/ml. Cells are then mixed with test agonist molecules and light emission by the aequorin is recorded with a luminometer for 30 seconds. Results are expressed as Relative Light Units (RLU). Controls include assays using membranes isolated from cells not expressing T1R or T2R (mock transfected), in order to exclude possible non-specific effects of the candidate compound.

[00158] Aequorin activity or intracellular calcium levels are "changed" if light intensity increases or decreases by 10% or more in a sample of cells, expressing a T1R or T2R polypeptide and treated with a candidate modulator, relative to a sample of cells expressing the T1R or T2R polypeptide but not treated with the candidate modulator or relative to a sample of cells not expressing the T1R or T2R polypeptide (mock-transfected cells) but treated with the candidate modulator.

[00159] ii) Adenylate Cyclase Assay:

[00160] Assays for adenylate cyclase activity are described by Kenimer & Nirenberg, Mol. Pharmacol. 20: 585-591 (1981) **(133)**. That assay is a modification of the assay taught by Solomon et al., 1974, Anal. Biochem. 58: 541-548 (1974) **(134)**, also incorporated herein by reference. Briefly, 100µl reactions contain 50 mM Tris-Hcl (pH 7.5), 5 mM $MgCl_2$, 20 mM creatine phosphate (disodium salt), 10 units (71 .µg of protein) of creatine phosphokinase, 1 mM α-^{32P} (tetrasodium salt, 2µCi), 0.5 mM cyclic AMP, G-^{3H}-labeled cyclic AMP (approximately 10,000 cpm), 0.5 mM Ro20-1724, 0.25% ethanol, and 50-200 µg of protein homogenate to be tested (i.e., homogenate from cells expressing or not expressing a T1R or T2R polypeptide, treated or not treated with a candidate modulator). Reaction mixtures are generally incubated at 37°C. for 6 minutes. Following incubation, reaction mixtures are deproteinized by the addition of 0.9 ml of cold 6% trichloroacetic acid. Tubes are centrifuged at 1800xg for 20 minutes and each supernatant solution is added to a Dowex AG50W-X4 column. The cAMP fraction from the column is eluted with 4 ml of 0.1 mM imidazole-HCl (pH 7.5) into a counting vial. Assays should be performed in triplicate. Control reactions should also be performed using protein homogenate from cells that do not express a T1R or T2R polypeptide.

[00161] According to the invention, adenylate cyclase activity is "changed" if it increases or decreases by 10% or more in a sample taken from cells treated with a candidate modulator of T1R or T2R activity, relative to a similar sample of cells not treated with the candidate modulator or relative to a sample of cells not

expressing the T1R or T2R polypeptide (mock-transfected cells) but treated with the candidate modulator.

[00162] iii) *cAMP Assay*:

[00163] Intracellular or extracellular cAMP is measured using a cAMP radioimmunoassay (RIA) or cAMP binding protein according to methods widely known in the art. For example, Horton & Baxendale, *Methods Mol. Biol.* 41: 91-105 (1995) **(135)**, which is incorporated herein by reference, describes an RIA for cAMP.

[00164] A number of kits for the measurement of cAMP are commercially available, such as the High Efficiency Fluorescence Polarization-based homogeneous assay marketed by LJL Biosystems and NEN Life Science Products. Control reactions should be performed using extracts of mock-transfected cells to exclude possible non-specific effects of some candidate modulators.

[00165] The level of cAMP is "changed" if the level of cAMP detected in cells, expressing a T1R or T2R polypeptide and treated with a candidate modulator of T1R or T2R activity (or in extracts of such cells), using the RIA-based assay of Horton & Baxendale, 1995 **(135)**, increases or decreases by at least 10% relative to the cAMP level in similar cells not treated with the candidate modulator.

[00166] (iv) Phospholipid Breakdown, DAG Production and Inositol Triphosphate Levels:

[00167] Receptors that activate the breakdown of phospholipids can be monitored for changes due to the activity of known or suspected modulators of T1R or T2R by monitoring phospholipid breakdown, and the resulting production of second messengers DAG and/or inositol triphosphate (IP_3). Methods of detecting each of these are described in Phospholipid Signalling Protocols, edited by Ian M. Bird. Totowa, N.J., Humana Press, (1998) **(136)**, which is incorporated herein by reference. See also Rudolph et al., *J. Biol. Chem.* 274: 11824-11831 (1999) **(137),** which also describes an assay for phosphatidylinositol breakdown. Assays should be performed using cells or extracts of cells expressing T1R or T2R, treated or not treated or without a candidate modulator. Control reactions should be performed using mock-transfected cells, or extracts from them in order to exclude possible non-specific effects of some candidate modulators.

[00168] According to the invention, phosphatidylinositol breakdown, and diacylglycerol and/or inositol triphosphate levels are "changed" if they increase or decrease by at least 10% in a sample from cells expressing a T1R or T2R polypeptide and treated with a candidate modulator, relative to the level observed in a sample from cells expressing a T1R or T2R polypeptide that is not treated with the candidate modulator.

[00169] (v) PKC Activation Assays:

[00170] Growth factor receptor tyrosine kinases can signal via a pathway involving activation of Protein Kinase C (PKC), which is a family of phospholipid- and calcium-activated protein kinases. PKC activation ultimately

results in the transcription of an array of proto-oncogene transcription factor-encoding genes, including c-fos, c-myc and c-jun, proteases, protease inhibitors, including collagenase type I and plasminogen activator inhibitor, and adhesion molecules, including intracellular adhesion molecule I (ICAM I). Assays designed to detect increases in gene products induced by PKC can be used to monitor PKC activation and thereby receptor activity. In addition, the activity of receptors that signal via PKC can be monitored through the use of reporter gene constructs driven by the control sequences of genes activated by PKC activation. This type of reporter gene-based assay is discussed in more detail below.

[00171] For a more direct measure of PKC activity, the method of Kikkawa et al., 1982, J. Biol. Chem. 257: 13341 (1982) **(138)**, can be used. This assay measures phosphorylation of a PKC substrate peptide, which is subsequently separated by binding to phosphocellulose paper. This PKC assay system can be used to measure activity of purified kinase, or the activity in crude cellular extracts. Protein kinase C sample can be diluted in 20 mM HEPES/2 mM DTT immediately prior to assay.

[00172] The substrate for the assay is the peptide Ac-FKKSFKL-NH_2, derived from the myristoylated alanine-rich protein kinase C substrate protein (MARCKS). The K_m of the enzyme for this peptide is approximately 50 μM. Other basic, protein kinase C-selective peptides known in the art can also be used, at a concentration of at least 2-3 times their K_m. Cofactors required for the assay include calcium, magnesium, ATP, phosphatidylserine and diacylglycerol. Depending upon the intent of the user, the assay can be performed to determine

the amount of PKC present (activating conditions) or the amount of active PKC present (non-activating conditions). For most purposes according to the invention, non-activating conditions will be used, such that the PKC, that is active in the sample when it is isolated, is measured, rather than measuring the PKC that can be activated. For non-activating conditions, calcium is omitted from the assay in favor of EGTA.

[00173] The assay is performed in a mixture containing 20 mM HEPES, pH 7.4, 1-2 mM DTT, 5 mM $MgCl_2$, 100μM ATP, .about. 1μCi .γ^{32}P-ATP, 100μg/ml peptide substrate (~100μM), 140μM/3.8μM phosphatidylserine/diacylglycerol membranes, and 100μM calcium (or 500μM EGTA). 48μL of sample, diluted in 20 mM HEPES, pH 7.4, 2 mM DTT is used in a final reaction volume of 80μl. Reactions are performed at 30°C for 5-10 minutes, followed by addition of 25μl of 100 mM ATP, 100 mM EDTA, pH 8.0, which stops the reactions.

[00174] After the reaction is stopped, a portion (85μl) of each reaction is spotted onto a Whatman P81 cellulose phosphate filter, followed by washes: four times 500 ml in 0.4% phosphoric acid, (5-10 min per wash); and a final wash in 500 ml 95% EtOH, for 2-5 min. Bound radioactivity is measured by scintillation counting. Specific activity (cpm/nmol) of the labelled ATP is determined by spotting a sample of the reaction onto PS1 paper and counting without washing. Units of PKC activity, defined as nmol phosphate transferred per min, are then calculated by known methods.

[00175] An alternative assay can be performed using a Protein Kinase C Assay Kit sold by PanVera (Cat. # P2747).

[00176] Assays are performed on extracts from cells expressing a T1R or T2R polypeptide, treated or not treated with a candidate modulator. Control reactions should be performed using mock-transfected cells, or extracts from them in order to exclude possible non-specific effects of some candidate modulators.

[00177] According to the invention, PKC activity is "changed" by a candidate modulator when the units of PKC measured by either assay described above increase or decrease by at least 10%, in extracts from cells expressing T1R or T2R and treated with a candidate modulator, relative to a reaction performed on a similar sample from cells not treated with a candidate modulator.

[00178] (iv) Kinase Assays:

[00179] MAP Kinase assays have already been described supra. MAP kinase activity can be assayed using any of several kits available commercially, for example, the p38 MAP Kinase assay kit sold by New England Biolabs (Cat # 9820) or the FlashPlate™ MAP Kinase assays sold by Perkin-Elmer Life Sciences.

[00180] MAP Kinase activity is "changed" if the level of activity is increased or decreased by 10% or more in a sample from cells, expressing a T1R or T2R polypeptide, treated with a candidate modulator relative to MAP kinase activity in a sample from similar cells not treated with the candidate modulator.

[00181] Direct assays for tyrosine kinase activity using known synthetic or natural tyrosine kinase substrates and labelled phosphate are well known, as are similar assays for other types of kinases (e.g., Ser/Thr kinases). Kinase assays can be performed with both purified kinases and crude extracts prepared from cells expressing a T1R or T2R polypeptide, treated with or without a candidate modulator. Control reactions should be performed using mock-transfected cells, or extracts from them in order to exclude possible non-specific effects of some candidate modulators. Substrates can be either full-length protein or synthetic peptides representing the substrate. Pinna & Ruzzene (Biochem. Biophys. Acta 1314: 191-225 (1996) **(139)**) list a number of phosphorylation substrate sites useful for detecting kinase activities. A number of kinase substrate peptides are commercially available. One that is particularly useful is the "Src-related peptide," RRLIEDAEYAARG (available from Sigma # A7433), which is a substrate for many receptor and nonreceptor tyrosine kinases. Because the assay described below requires binding of peptide substrates to filters, the peptide substrates should have a net positive charge to facilitate binding. Generally, peptide substrates should have at least 2 basic residues and a free amino terminus. Reactions generally use a peptide concentration of 0.7-1.5 mM.

[00182] Assays are generally carried out in a 25 µl volume comprising 5 .mu.l of 5X kinase buffer (5 mg/mL BSA, 150 mM Tris-Cl (pH 7.5), 100 mM $MgCl_2$; depending upon the exact kinase assayed for, $MnCl_2$ can be used in place of or in addition to the $MgCl_2$), 5 .mu.l of 1.0 mM ATP (0.2 mM final concentration), γ^{32}P-ATP (100-500 cpm/pmol), 3µl of 10 mM peptide substrate (1.2 mM final

concentration), cell extract containing kinase to be tested (cell extracts used for kinase assays should contain a phosphatase inhibitor (e.g. 0.1-1 mM sodium orthovanadate)), and H_2O to 25µl. Reactions are performed at 30°C., and are initiated by the addition of the cell extract.

[00183] Kinase reactions are performed for 30 seconds to about 30 minutes, followed by the addition of 45µl of ice-cold 10% trichloroacetic acid (TCA). Samples are spun for 2 minutes in a microcentrifuge, and 35µl of the supernatant is spotted onto Whatman P81 cellulose phosphate filter circles. The filters are washed three times with 500 ml cold 0.5% phosphoric acid, followed by one wash with 200 ml of acetone at room temperature for 5 minutes. Filters are dried and incorporated ^{32}P is measured by scintillation counting. The specific activity of ATP in the kinase reaction (e.g., in cpm/pmol) is determined by spotting a small sample (2-5µl) of the reaction onto a P81 filter circle and counting directly, without washing. Counts per minute obtained in the kinase reaction (minus blank) are then divided by the specific activity to determine the moles of phosphate transferred in the reaction.

[00184] Tyrosine kinase activity is "changed" if the level of kinase activity is increased or decreased by 10% or more in a sample from cells, expressing a T1R or T2R polypeptide, treated with a candidate modulator relative to kinase activity in a sample from similar cells not treated with the candidate modulator.

[00185] (vii) Transcriptional Reporters for Downstream Pathway Activation:

[00186] The intracellular signal initiated by binding of an agonist to a receptor, e.g., T1R or T2R, sets in motion a cascade of intracellular events, the ultimate consequence of which is a rapid and detectable change in the transcription or translation of one or more genes. The activity of the receptor can therefore be monitored by detecting the expression of a reporter gene driven by control sequences responsive to T1R or T2R activation.

[00187] As used herein "promoter" refers to the transcriptional control elements necessary for receptor-mediated regulation of gene expression, including not only the basal promoter, but also any enhancers or transcription-factor binding sites necessary for receptor-regulated expression. By selecting promoters that are responsive to the intracellular signals resulting from agonist binding, and operatively linking the selected promoters to reporter genes whose transcription, translation or ultimate activity is readily detectable and measurable, the transcription based reporter assay provides a rapid indication of whether a given receptor is activated.

[00188] Reporter genes such as luciferase, CAT, GFP, β-lactamase or β-galactosidase are well known in the art, as are assays for the detection of their products.

[00189] Genes particularly well suited for monitoring receptor activity are the "immediate early" genes, which are rapidly induced, generally within minutes of contact between the receptor and the effector protein or ligand. The induction of immediate early gene transcription does not require the synthesis of new

regulatory proteins. In addition to rapid responsiveness to ligand binding, characteristics of preferred genes useful for making reporter constructs include: low or undetectable expression in quiescent cells; induction that is transient and independent of new protein synthesis; subsequent shut-off of transcription requires new protein synthesis; and mRNAs transcribed from these genes have a short half-life. It is preferred, but not necessary that a transcriptional control element have all of these properties for it to be useful.

[00190] An example of a gene that is responsive to a number of different stimuli is the c-fos proto-oncogene. The c-fos gene is activated in a protein-synthesis-independent manner by growth factors, hormones, differentiation-specific agents, stress, and other known inducers of cell surface proteins. The induction of c-fos expression is extremely rapid, often occurring within minutes of receptor stimulation. This characteristic makes the c-fos regulatory regions particularly attractive for use as a reporter of receptor activation.

[00191] The c-fos regulatory elements include (see, Verma et al., Cell 51: 513-514) (1987) **(140)**: a TATA box that is required for transcription initiation; two upstream elements for basal transcription, and an enhancer, which includes an element with dyad symmetry and which is required for induction by TPA, serum, EGF, and PMA.

[00192] The 20 bp c-fos transcriptional enhancer element located between -317 and -298 bp upstream from the c-fos mRNA cap site, is essential for serum induction in serum starved NIH 3T3 cells. One of the two upstream elements is

located at -63 to -57 and it resembles the consensus sequence for cAMP regulation.

[00193] The transcription factor CREB (cyclic AMP responsive element binding protein) is, as the name implies, responsive to levels of intracellular cAMP. Therefore, the activation of a receptor that signals via modulation of cAMP levels can be monitored by detecting either the binding of the transcription factor, or the expression of a reporter gene linked to a CREB-binding element (termed the CRE, or cAMP response element). The DNA sequence of the CRE is TGACGTCA. (Reporter constructs responsive to CREB binding activity are described in U.S. Pat. No. 5,919,649) **(141)**.

[00194] Other promoters and transcriptional control elements, in addition to the c-fos elements and CREB-responsive constructs, include the vasoactive intestinal peptide (VIP) gene promoter (cAMP responsive; Fink et al., 1988, *Proc. Natl. Acad. Sci.* 85:6662-6666) (1988) **(142)**; the somatostatin gene promoter (cAMP responsive; Montminy et al., *Proc. Natl. Acad. Sci.* 83:6682-6686 (1986) **(143)**); the proenkephalin promoter (responsive to cAMP, nicotinic agonists, and phorbol esters; Comb et al., *Nature* 323:353-356 (1986) **(144)**); the phosphoenolpyruvate carboxy-kinase (PEPCK) gene promoter (cAMP responsive; Short et al., *J. Biol. Chem.* 261:9721-9726 (1986) **(145)**).

[00195] Additional examples of transcriptional control elements that are responsive to changes in GPCR activity include, but arc not limited to those responsive to the AP-1 transcription factor and those responsive to NF-KB

activity. The consensus AP-1 binding site is the palindrome TGA(C/G)TCA (Lee et al., *Nature* 325: 368-372 (1987) **(146)**; Lee et al., *Cell* 49: 741-752 (1987) **(147)**). The AP-1 site is also responsible for mediating induction by tumor promoters such as the phorbol ester 12-O-tetradecanoylphorbol-.beta.-acetate (TPA), and are therefore sometimes also referred to as a TRE, for TPA-response element. AP-1 activates numerous genes that are involved in the early response of cells to growth stimuli. Examples of AP-1-responsive genes include, but are not limited to the genes for Fos and Jun (which proteins themselves make up AP-1 activity), Fos-related antigens (Fra) 1 and 2, I κβα, ornithine decarboxylase, and annexins I and II.

[00196] The NF-KB binding element has the consensus sequence GGGGACTTTCC. A large number of genes have been identified as NF-KB responsive, and their control elements can be linked to a reporter gene to monitor GPCR activity. A small sample of the genes responsive to NF-KB includes those encoding IL-1β. (Hiscott et al., *Mol. Cell. Biol.* 13:6231-6240 (1993) **(148)**), TNF-α (Shakhov et al., *J. Exp. Med.* 171: 35-47 (1990) **(149)**), CCR5 (Liu et al., AIDS Res. Hum. Retroviruses 14: 1509-1519 (1998) **(150)**), P-selectin (Pan & McEver, *J. Biol. Chem.* 270: 23077-23083 (1995) **(151)**), Fas ligand (Matsui et al., *J. Immunol.* 161: 3469-3473 (1998) **(152)**), GM-CSF (Schreck & Baeuerle, *Mol. Cell. Biol.* 10: 1281-1286 (1990) **(153)**) and Iκβα (Haskill et al., *Cell* 65: 1281-1289 (1991) **(154)**). Vectors encoding NF-KB-responsive reporters are also known in the art or can be readily made by one of skill in the art using, for example, synthetic NF-KB elements and a minimal promoter, or using the NF-

KB-responsive sequences of a gene known to be subject to NF-KB regulation. Further, NF-KB responsive reporter constructs are commercially available *e.g.*, from CLONTECH.

[00197] To screen for agonists, the cells are left untreated, exposed to candidate modulators, and expression of the reporter is measured. An increase of at least 50% in reporter expression in the presence of a candidate modulator indicates that the candidate is a modulator of T1R or T2R activity. An agonist will induce at least as many, and preferably the same amount or more of reporter expression than buffer alone. This approach can also be used to screen for inverse agonists where cells express a T1R or T2R polypeptide at levels such that there is an elevated basal activity of the reporter. A decrease in reporter activity of 10% or more in the presence of a candidate modulator, relative to its absence, indicates that the compound is an inverse agonist.

[00198] To screen for antagonists, the cells expressing T1R or T2R and carrying the reporter construct are contacted in the presence and absence of a candidate modulator. A decrease of 10% or more in reporter expression in the presence of candidate modulator, relative to the absence of the candidate modulator, indicates that the candidate is a modulator of T1R or T2R activity.

[00199] Controls for transcription assays include cells not expressing T1R or T2R but carrying the reporter construct, as well as cells with a promoterless reporter construct. Compounds that are identified as modulators of T1R or T2R-regulated transcription should also be analyzed to determine whether they affect

transcription driven by other regulatory sequences and by other receptors, in order to determine the specificity and spectrum of their activity.

[00200] The transcriptional reporter assay, and most cell-based assays, are well suited for screening expression libraries for proteins for those that modulate T1R or T2R activity. The libraries can be, for example, cDNA libraries from natural sources, e.g., plants, animals, bacteria, etc., or they can be libraries expressing randomly or systematically mutated variants of one or more polypeptides. Genomic libraries in viral vectors can also be used to express the mRNA content of one cell or tissue, in the different libraries used for screening of T1R or T2R.

[00201] (viii) Inositol Phosphate (IP) Measurement:

[00202] Cells of the invention are labelled for 24 hours with 10μCi/ml^{3}H] inositol in inositol free DMEM containing 5% FCS, antibiotics, amphotericin, sodium pyruvate and 400 μg/ml G418. Cells are incubated for 2 h in Krebs-Ringer Hepes (KRH) buffer of the following composition (124 mM NaCl, 5 mM KCl, 1.25 mM $MgSO_4$, 1.45 mM $CaCl_2$, 1.25 mM KH_2PO_4, 25 mM Hepes (pH:7.4) and 8 mM glucose). The cells are then challenged with various nucleotides for 30 s. The incubation is stopped by the addition of an ice cold 3% perchloric acid solution. IP are extracted and separated on Dowex columns as previously described. 2MeSATP and ATP solutions (1 mM) are treated at room temperature with 20 units/ml CPK and 10 Mm cp for 90 min to circumvent problems arising from the contamination and degradation of triphosphate nucleotide solutions.

[00203] T1R or T2R Assay

[00204] The invention provides for an assay for detecting the activity of a receptor of the invention in a sample. For example, T1R or T2R activity can be measured in a sample comprising a cell or a cell membrane that expresses T1R or T2R. The assay is performed by incubating the sample in the presence or absence of a modulator and carrying out a second messenger assay, as described above. The results of the second messenger assay performed in the presence or absence of the activator are compared to determine if the T1R or T2R receptor is active.

[00205] Any of the assays of receptor activity, including but not limited to the GTP-binding, GTPase, adenylate cyclase, cAMP, phospholipid-breakdown, diacylglycerol, inositol triphosphate, arachidonic acid release (see below), PKC, kinase and transcriptional reporter assays, can be used to determine the presence of an agent in a sample, e.g., a tissue sample, that affects the activity of the T1R or T2R receptor molecule. To do so, T1R or T2R polypeptide is assayed for activity in the presence and absence of the sample or an extract of the sample. An increase in T1R or T2R activity in the presence of the sample or extract relative to the absence of the sample indicates that the sample contains an agonist of the receptor activity. A decrease in receptor activity in the presence of an agonist and the sample, relative to receptor activity in the absence thereof, indicates that the sample contains an antagonist of T1R or T2R activity.

[00206] The amount of increase or decrease in measured activity necessary for a sample to be said to contain a modulator depends upon the type of assay used. Generally, a 10% or greater change (increase or decrease) relative to an assay

performed in the absence of a sample indicates the presence of a modulator in the sample. One exception is the transcriptional reporter assay, in which at least a two-fold increase or 10% decrease in signal is necessary for a sample to be said to contain a modulator. It is preferred that an agonist stimulates at least 50%, and preferably 75% or 100% or more, e.g., 2-fold, 5-fold, 10-fold or greater receptor activation.

[00207] Other functional assays include, for example, microphysiometer or biosensor assays (see Hafner, 2000, Biosens. Bioelectron. 15: 149-158) (2000) **(155)**).

[00208] As described in detail *infra,* it has been found that cell-based assays according to the invention, *e.g.,* MAPK and cAMP assay methods exemplified, enable the detection of robust activation of bitter taste receptors (mT2R05) and hT2R04 as well as the sweet receptor (T1R2/T1R3) and umami receptor (T1R1/T1R3). (These results are discussed in detail in the examples and the figures referred to therein.) It is anticipated further, based on these results, that cell-based assays that detect the effect of putative modulator on G_i/T1R or G_i/TR mediated signaling pathways, *e.g.,* MAPK and cAMP assays, will be identify compounds that modulate the activity of any functional taste receptor comprising a T1R or T2R polypeptide or functional fragment.

[00209] Additionally, the results obtained indicate that the responses obtained are receptor-dependent and receptor-specific. For example, the parental cell lines

HEK293 or HEK293T-G_{15} do not exhibit comparable activation of MAPK or a reduction in cAMP (*See* **Figures 1-7**) when stimulated with the same agonists.

[00210] Further, it has been found that treatment of taste-receptor expressing cells with pertussis toxin (PTX), which blocks functional coupling between GPCRs and Gi proteins, prevents MAPK activation and prevents a decrease in cAMP accumulation. These results indicate that the subject MAPK and cAMP assay systems provide an efficient means for identifying compounds that modulate, *e.g.*, enhance, agonize or antagonize the activity of specific taste receptors i.e., T1R2/T1R3 (sweet receptor) or T1R1/T1R3 (umami receptors) or specific T2Rs (bitter receptors).

[00211] The subject MAPK assays are exemplified by the above-described antibody-based methods for detecting MAPK activation. As noted supra, however, the invention encompasses any suitable assay system for detecting activated MAPK. **(71)** Vaster et al., *Biochem J.* 350:717-22 (2000), incorporated by reference in its entirety herein, describes a phosphospecific cell-based ELISA for detecting p42/p44 MAPK, p38MAPK, protein kinase B and cAMP response-element binding protein. This assay, referred to as "PACE", (phosphospecific antibody cell-based ELISA) detects activated MAPK without the use of radioactive labels, and can use adherent cells or cells in suspension.

[00212] Alternatively, the detection of MAPK activation can be effected by the use of proximity assays (AlphaScreenTM) from Packard or by use of High Content Screen System (ERK MAPK Activation HitKit™) from Cellomics. These

assays or other available MAPK assays, can be used as part of a high throughput screening platform for identifying bitter, sweet and umami receptor agonists and antagonists.

[00213] In the preferred embodiment, cAMP accumulation is measured by an immunofluorescence assay as described in the examples. However, as noted supra, the subject invention embraces the use of any suitable means for detecting cAMP levels. Such methods include the detection of cAMP using anti-cAMP antibodies in an ELISA-based format, or by second messenger reporter system assays. Promoters on genes drive the expression of the proteins that a particular gene encodes. Cyclic AMP drives gene expression by promoting the binding of a cAMP-responsive DNA binding protein or transcription factor (CREB) that then binds to the promoter at specific sites called cAMP response elements and drives the expression of the gene. As discussed supra, reporter systems can be constructed which have a promoter containing multiple cAMP response elements before a reporter gene, *e.g.*, beta-galactosidose or luciferase. In this assay, a constitutively activated G_i linked receptor causes a reduction in cAMP that results in inhibition of the gene expression and reduced expression of the reporter gene. The reporter protein can be detected using standard biochemical assays.

Functional Coupling of G_i Proteins to T1Rs and T2Rs

[00214] In another aspect, the present invention relates to the discovery that T1Rs and T2Rs functionally couple to G proteins other than promiscuous G proteins such as $G\alpha_{15}$ or gustducin. Particularly, the invention involves the

discovery that T1Rs and T2Rs functionally couple to G_i proteins and use $G_{\alpha i}$ to transmit signals to downstream effectors, *e.g.,* adenylyl cyclase and MAP Kinase.

[00215] G_s stimulates the enzyme adenylyl cyclase . By contrast, G_i (and G_z and G_0) inhibit this enzyme. Adenylyl cyclase catalyzes the conversion of ATP to cAMP. Thus, constitutively activated GPCRs that couple G_i (or G_z and G_0) protein associated with a decrease in cellular levels of cAMP. *See, generally,* "Indirect Mechanisms of Synoptic Transmission," Chapter 8, From *Neuron to Brain (3rd Edition), Nichols, J.G. et al etds.,* Sinaver Associates, Inc. (1992). Thus, assays that detect cAMP can be utilized to determine if a compound is *e.g.,* an inverse agonist to the receptor (*i.e.*, such a compound would decrease the levels of cAMP): As noted previously, a variety of approaches can be used to measure cAMP, *e.g.*, anti-cAMP antibodies in an ELISA method, or the second messenger reporter system assays described *supra.*

[00216] As noted, a G_i protein coupled receptor is known to inhibit adenylyl cyclase, resulting in a decrease in cAMP production. Another effective technique for measuring the decrease in production of cAMP as an indication of constitutive activation of a receptor that predominantly couples G_i upon activation can be accomplished by co-transfecting a signal enhancer, *e.g.*, a non-endogenous, constitutively activated receptor that predominantly couples with G_s upon activation with the G_i linked GPCR, *i.e.,* a T1R or T2R. In contrast to G_i coupled GPCRs, constitutive activation of a G_s coupled receptor can be determined based upon an increase in production of cAMP. Thus, this construction approach is intended to advantageously exploit these "opposite"

effects. For example, co-transfection of a non-endogenous, constitutively activated G_s coupled receptor ("signal enhancer") with the G_i coupled receptor (T1R or T2R) provides a baseline cAMP signal (*i.e.*, although the G_i coupled receptor will decrease cAMP levels, this "decrease" will be relative to the substantial increase in cAMP levels established by constitutively activated G_s coupled signal enhancer). By then co-transfecting the signal enhancer with a constitutively activated version of the target receptor, cAMP will decrease further (relative to the baseline) due to the increased functional activity of the G_i target, *i.e.*, T1R or T2R, which decreases cAMP.

[00217] Screening for potential T1R or T2R modulators using such a cAMP assay can then be accomplished with two provisos: first, relative to the G_i coupled target receptor (T1R or T2R), "opposite" effects will result, *i.e.*, an inverse agonist of the G_i coupled target receptor will decrease this signal; second candidate modulators that are identified using this approach should be assessed independently to ensure that these compounds do not target the signal enhancing receptor (this can be accomplished prior to or after screening against co-transfected receptor).

[00218] Additionally, as described above, other assays can be designed which assess the effects of cAMP on other cellular events. Alteration of the intracellular concentration of cAMP is known to affect many cellular reactions. For example, an increase in cAMP intracellular concentrations stimulates the activity of protein Kinases. For a general review of cAMP and secondary

messenger systems associated therewith, reference is made to "Molecular Cell Biology", Darnell et al, Chapter 16 (1986) **(156)**.

[00219] Particular signal substances that use cAMP as a second messenger include by way of example calcitonin, chorionic gonadotropin, corticotrophin, epinephrine, follicle-stimulating homone, glucagon, leutenizing hormone, lipotropin, melanocyte-stimulating hormone, norepinephrine, parathyroid hormone (PTH), thyroid-stimulating hormone and vasopressin.

[00220] The subject assays which measure the effect of a putative modulator or TR/G_i associated signaling pathways were not suggested by the state of the art. In vivo, receptors for bitter and sweet taste functionally couple to the taste-specific G-protein α-gustducin to initiate the transduction cascade leading to taste perception. In heterologous cells, however, previously there was no direct evidence of functional coupling to G-proteins other than $G\alpha_{15}$, a promiscuous G-protein widely used for receptor deorphaning. Unexpectedly, the present inventors have demonstrated that receptors for bitter, sweet and also umami taste couple effectively to G_i-signaling pathways when expressed in human embryonic kidney cells. For example, cycloheximide, a bitter compound, specifically activates ERK1/2 mitogen-activated kinases in cells expressing the mouse bitter receptor mT2R5 and the rat bitter receptors rT2R9. Consistent with the foregoing, activation of ERK1/2 is totally abolished upon treatment with pertussis toxin indicating that these receptors couple to ERK1/2 activation through $G\alpha_i$. Also in agreement with these observations, cycloheximide inhibits the forskolin-induced cAMP accumulation in mT2R5-expressing cells by 70%.

Similarly, as shown *infra* in the examples, natural and artificial sweeteners such as sucrose, D-tryptophan, saccharin and cyclamate (known activates of T1R2/T1R3 sweet receptors) activate ERK1/2 in cells expressing the human sweet receptor hT1R2/hT1R3. Also, as shown in detail *infra,* monosodium glutamate exclusively activates ERK1/2 in cells expressing the human umami receptor hT1R1/hT1R3 and the effect is greatly enhanced by the presence of inosine monophosphate. Again, consistent with Gi coupling, these responses are prevented by treatment with pertussis toxin.

[00221] Further, as shown in detail *infra,* sweeteners including cyclamate, aspartame, saccharin, and monellin significantly inhibit the forskolin-induced cAMP accumulation in hT1R2/hT1R3-expressing cells by 50-70%. Monosodium glutamate also decreases basal levels of cAMP in hT1R1/hT1R3-expressing cells by 50%.

[00222] While the results obtained are unexpected, some earlier information relating to taste-specific GPCRs is consistent with these results. Particularly it was known that taste-specific GPCRs use heterotrimeric G proteins to relay intracellular signals leading to cell depolarization and, subsequently, taste perception. Also, it was known that deletion of the gene encoding a taste-specific G protein subunit, α-gustducin **(73)** (McLaughlin et al., *Nature* 357:563-569 (1992)), produces mice that are defective in detection of bitter and sweet substances **(17)**. The visual G-protein α-transducin is also expressed in taste tissue **(74, 75)** (Ruiz-Avila et al., *Nature* 376:80-85 (1995); McLaughlin et al., *Phys. Behav.* 56(6):1157-64 (1994)) and its selective expression in α-gustducin

deficient TRCs partially rescues the tasting phenotype to sweet and bitter substances **(27)** He et al, *Chem. Senses*, 27(8): 719-27 (2002). In biochemical assays, bitter tasting substances activate α-gustducin **(127)** Ming et al., *Proc.. Natl Acad Sci, USA* 95(10): 8933-8 (1992) and α-transducin **(128)** Ruiz-Avila et al., *Chem Senses*, 20(4): 361-8 (2000). Similarly, cycloheximide induces α-gustducin activation in cell membranes derived from mT2R5-expressing cells Chandrashekar et al. *Cell* 100(6): 703-711 (2000) **(80)**.

[00223] It has also been suggested that taste GPCRs use G-proteins other than α-gustducin to relay intracellular signals and that TRCs express a vast repertoire of different G protein subunits. Expression of $G\alpha_s$, $G\alpha_{15}$, $G\alpha_{il-1}$,, $G\alpha_{il-2}$, $G\alpha_{l-3}$ and $G\alpha_q$ has been detected in taste tissues using RT-PCR **(15, 25)**. $G\alpha_{il-2}$ can also be detected by *in situ* hybridization (25, 26) and immunostaining **(25)** in TRCs and a study by Hoon et al., **(32)** reported that G_i proteins are expressed in almost all TRCs. As a result, $G\alpha_{il-2}$ positive cells are thought to be larger in number than Gα-gustducin-positive cells in rat circumvallate papillae (Kusakabe et al., *Chem. Senses* 25(5):525-31 (2000) **(25)**). Also, α-gustducin deficient mice retain residual responsiveness to bitter and sweet stimuli (Wong et al., *Nature* 381:796-800 (1996); He et al, *Chem Senses* 27(8): 719-27 (2002); Ruiz-Avila et al, *PNC Natl Acad Sci,* USA 98(15): 541-551 (2001) **(17, 27, 28)**) suggesting that another G protein may complement α-gustducin functions in TRCs.

[00224] Further, some earlier biochemical studies have suggested the possible existence of signaling pathways parallel to α-gustducin in TRCs. For example, the application of bitter-tasting substances (Yan et al, *Am J. Physiol Cell*

Physiol. 280(2): C742-751 (2001) **(76)**) to taste tissue reduces the levels of 3', 5'-cyclic nucleotide monophosphate (cAMP) in taste tissue papillae. By contrast, the application of sweeteners to taste tissue membranes has been reported to increase levels of cAMP Naim et al, *Comp. Biochem Physiol B* 100(3): 455-8 (1991); Striem et al, *Biochem J.* 260(1): 121-6 (1989) **(77, 78)**. However, prior to this invention there existed no direct evidence of functional coupling between taste GPCRs and G-proteins other than α-gustducin, α-transducin and $G\alpha_{15/16}$, a promiscuous G-protein widely used for receptor deorphaning **(79)** (Kostensis, *Trends Pharmacol Sci* 22(11) 560-564 (2001)). and none of these G-proteins were known to directly activate effectors capable of modulating the levels of cyclic nucleotides in TRCs.

[00225] Current models that do not take into account the experimental results herein suggested that the sweet taste receptor can also couple to $G\alpha_s$ and that α-gustducin activates, by unknown mechanisms, a taste specific cyclic nucleotide phosphodiesterase (PDE) **(9, 10)** (Gilbertson et al., *Curr. Opin. Neurobiol.* 10(4): 519-27 (2000); Margolskee, R. F., *J. Biol Chem* 277(1):1-4 (2002)). However, these hypothetical signaling pathways have not yet been definitely linked to taste receptor activation in TRCs or in fact any other cell types.

[00226] By contrast, the present inventors have studied coupling of receptors for bitter, sweet and umami taste to classical GPCR-linked signaling pathways in HEK293 cells, and the results obtained surprisingly demonstrate that these taste receptors can effectively couple to $G\alpha_i$-dependent activation of mitogen activated protein (MAP) kinases ERK1 and ERK2 (ERK1/2) and $G\alpha_i$-dependent

inhibition of cAMP accumulation. Also, these results further surprisingly indicate that the sweet receptor does not couple to G_s stimulation and accumulation of cAMP. Functional coupling to $G\alpha_i$ may explain, in part, the observations that bitter-tasting substances and MSG decrease the level of cyclic nucleotides in TRCs. Moreover, these results suggest that $G\alpha_i$ can functionally complement α-gustducin functions in TRCs.

Applications of the Subject Assays

[00227] The present invention provides cell-based assay methods that rely on the discovery that T1Rs and T2Rs functionally couple to G_i proteins *e.g.*, $G\alpha_i$ and transmit signals to downstream effectors, *e.g.*, cAMP, MAP Kinase, and adenylyl cyclase that enable the identification of modulators, *e.g.*, agonists, antagonists, inverse agonists enhancers of a T1R or T2R polypeptide. The T2R modulators of the invention are useful for altering taste perception, for example to induce, suppress or enhance bitter taste perception in a subject. The T1R2/T1R3 modulators are useful for modulating sweet taste, *e.g.*, by enhancing the taste of another sweet tasting compound such as saccharin. The T1R1/T1R3 modulators identified according to the invention are useful for modulating umami taste, *e.g.*, by enhancing the taste of a umami compound such as monosodium glutamate.

Compositions

[00228] In accordance with the methods of the present invention, a composition that is administered to alter taste perception in a subject will comprise an effective amount of a T1R or T2R modulator (agonist, antagonist, or enhancer). A T1R or T2R activator or modulator can comprise any substance *e.g.*, small

molecule, peptide, protein, carbohydrate, oligosaccharide, glycoprotein, amino acid derivative, and the like. In general, compounds will be identified by screening libraries of potential taste modulatory compounds, which may be comprised of synthetic or naturally occurring compounds. The library may be random or may comprise compounds having related structures or are structures or substitutions. After lead candidates are identified, compound libraries having similar structure will be produced and screened for T1R or T2R modulatory activity according to the invention. T1R or T2R modulators identified as disclosed herein can be used to prepare compositions suitable for oral use, including but not limited to food, beverages, oral washes, dentifrices, cosmetics, and pharmaceuticals. T1R or T2R modulators can also be used as additives to alter the sweet, umami or bitter taste of a compound that is of palatable but undesirable for oral use, for example compounds comprised in household cleansers, poisons, etc. Such modulators will alter bitter, sweet or umami tasting compounds contained therein.

[00229] For example, representative foods having an undesirable or bitter taste include, but are not limited to, citrus fruits such as grapefruit, orange, and lemon; vegetables such as tomato, pimento, celery, melon, carrot, potato, and asparagus; seasoning or flavoring materials such as flavor, sauces, soy sauce, and red pepper; foods originating from soybean; emulsion foods such as cream, dressing, mayonnaise, and margarine; processed marine products such as fish meat, ground fish meat, and fish eggs; nuts such as peanuts; fermented foods such as fermented soybean; meats and processed meats; pickles; noodles; soups

including powdery soups; dairy products such as cheese; breads and cakes; confectioneries such as candies, chewing gum, and chocolate; and specifically prepared foods for health.

[00230] Representative. cosmetics eliciting bitter taste (e.g., skin lotions, creams, face packs, lip sticks, foundations, shaving preparations, after-shave lotions, cleansing foams, and cleansing gels) include but are not limited to those compositions that include surfactants such as sodium alkyl sulfate and sodium monoalkyl phosphate; fragrances such as menthol, linalool, phenylethyl alcohol, ethyl propionate, geraniol, linalyl acetate and benzyl acetate; antimicrobials such as methyl paraben, propyl paraben and butyl paraben; humectants such as lactic acid and sodium lactate; alcohol-denaturating agents such as sucrose octaacetate and brucine; and astringents such as aluminum lactate.

[00231] Representative pharmaceuticals having a bitter taste include acetaminophen, terfenadine, guaifenesin, trimethoprim, prednisolone, ibuprofen, prednisolone sodium phosphate, methacholine, pseudoephedrine hydrochloride, phenothiazine, chlorpromazine, diphenylhydantoin, caffeine, morphine, demerol, codeine, lomotil, lidocaine, salicylic acid, sulfonamides, chloroquine, a vitamin preparation, minerals and penicillins. neostigmine, epinephrine, albuterol, diphenhydramine, chlorpheniramine maleate, chlordiazepoxide, amitriptyline, barbiturates, diphenylhydantoin, caffeine, morphine, demerol. codeine, lomotil, lidocaine, salicylic acid, sulfonamides, chloroquine, a vitamin preparation, minerals and penicillins.

[00232] Representative sweeteners which may be modulated by compounds according to the invention include xylitol, sorbitol, saccharin, sucrose, glucose, fructose, cyclamate, aspartame, monellin, and the like, and derivatives thereof.

[00233] Representative umami compounds, the taste which may be modulated according to the invention include L-glutamate, L-asparate, monosodium glutamate, derivatives thereof, compounds containing and the like.

[00234] These taste modulators can also be administered as part of prepared food, beverage, oral wash, dentifrice, cosmetic, or drug. To prepare a composition suitable for administration to a subject, a T1R or T2R modulator can be admixed with a compound, the taste of which is to be modulated in amount comprising about 0.001 % to about 10% by weight, preferably from about 0.01% to about 8% by weight, more preferably from about 0.1 % to about 5% by weight, and most preferably from about 0.5% to about 2% by weight.

[00235] Suitable formulations include solutions, extracts, elixirs, spirits, syrups, suspensions, powders, granules, capsules, pellets, tablets, and aerosols. Optionally, a formulation can include a pharmaceutically acceptable carrier, a suspending agent, a solubilizer, a thickening agent, a stabilizer, a preservative, a flavor, a colorant, a sweetener, a perfume, or a combination thereof. T1R or T2R modulators and compositions can be presented in unit-dose or multi-dose sealed containers, such as ampules and vials.

Administration

[00236] T1R or T2R modulators can be administered directly to a subject for modulation of taste perception. Preferably, a modulator of the invention is administered orally or nasally.

[00237] In accordance with the methods of the present invention, an effective amount of a T1R or T2R modulator is administered to a subject. The term "effective amount" refers to an amount of a composition sufficient to modulate T1R or T2R activation and/or to modulate taste perception, e.g., bitter, sweet or umami taste perception.

[00238] An effective amount can be varied so as to administer an amount of an T1R or T2R modulator that is effective to achieve the desired taste perception. The selected dosage level will depend upon a variety of factors including the activity of the T1R or T2R modulator, formulation, combination with other compositions (e.g., food, drugs, etc.), the intended use (e.g., as a food additive, dentifrice, etc.), and the physical condition and prior medical history of the subject being treated.

[00239] An effective amount or dose can be readily determined using in vivo assays of taste perception as are known in the art. Representative methods for assaying taste perception are described *infra*.

EXAMPLES

[00240] The invention is further illustrated by the following non-limiting examples wherein the following materials and methods are used.

Materials and Methods

[00241] Sweeteners, agonists and toxins. Sucrose, aspartame, cyclamate, monellin, monosodium glutamate, inosine monophosphate, isoproterenol, epidermal growth factor, denatonium benzoate, quinine sulfate, cycloheximide, rolipram and forskolin were from Sigma (St-Louis, MO). Pertussis toxin (PTX) was from List Biological Laboratories (Campbell, CA).

[00242] Establishment of stable cell lines. An inducible expression system was used for the umami taste receptor line (hT1R1/hT1R3). Vectors were prepared using the GeneSwitch inducible system (Invitrogen, Carlsbad, CA). hT1R1 and hT1R3 vectors were prepared by cloning receptor cDNA into pGene/V5-His A at EcoRI/Not I sites. A modified pSwitch vector was also prepared by replacing the hygromycin β resistance gene with the puromycin resistance gene. The cDNAs for hT1R1, hT1R3, and puromycin resistance were co-transfected into HEK293 cells stably expressing $G\alpha_{15}$ (Aurora Biosciences, San Diego, (80) Chandraskekar et al, *Cell* 100(6): 703-11 (2000). hT1R1/hT1R3 stable cell lines were selected and maintained in high-glucose DMEM media containing 100μg/mL zeocin, 0.5μg/mL puromycin, 2mM GIutaMAX 1, 10% dialyzed fetal bovine serum, 3μg/mL blasticidin and penicillin/streptomyocin. To improve cell adhesion, cell flasks were pre-coated with Matrigel (Becton-Dickinson, Bedford, MA) at a dilution of 1:400. Expression of hT1R1 and hT1R3 was induced by treatment of cells with $6x10^{-11}$M mifepristone for 48 hours prior to experiments. Clones were tested and selected for mifepristone-induced responsiveness to MSG/IMP using calcium-imaging experiments (data not

shown). The clone used in this study did not show any functional expression of hT1R1/R3 without induction (data not shown).

[00243] Establishment of the sweet (hT1R2/R3) receptor line stable cell line has already been described Li et al., *Proc. Natl Acad. Sci, USA* 99(7): 4692-6 (2002) **(14)**. Cells were maintained in low-glucose DMEM media containing 10% heat-inactivated dialyzed FIBS, penicillin/streptomyocin, 3 μg/mL blasticidin, 100ug/ml zeocin, and 0.5ug/ml puromycin in Matrigel-coated flasks.

[00244] HEK293 cells were transfected with 5 μg of linearized Rho-mT2R5 plasmid **(80)** Chandraskekar et al (2000) in pEAK10 (Edge biosystems) using the Transit transfection reagent (Panvera). Cells were selected in the presence of 0.5 μg/ml puromycin, clones were isolated, expanded and analyzed by fluorescence-activated cell sorting for the presence of Rho tag immunoreactivity at the cell surface using a monoclonal antibody; raised against the first 40 amino acids of rhodopsin **(80, 81)** (Chandrashekar et al (2000); Adamus et al., *Vision Res.* 31(1): 17-31 (1991)).

EXAMPLE 1

MAP Kinase Assays

[00245] Transient transfection of HEK293 cells for ERK112 assay. Subclonfluent HEK293 cells in 10cm dishes were transfected with 4 μg of Rho-rT2R9 plasmid (Chandrashekar et al (2000); Bufe et al., *J. Receptor Signal Transduct. Res.* 20(2-3): 153-166 (2000)) pEAK10 (Edge Biosystems, Gaithersburg, MD **(80, 82)**) and 2 μg pUC-18 as a carrier DNA using the Transit transfection reagent (Panvera). 24 hours later, cells were harvested using

Hank's balanced salt solution without calcium or magnesium and containing 1 mM EDTA (HBSS/EDTA), and plated into 6 well plates. ERK1/2 assay was performed 48 hours post-transfection.

[00246] Determination of ERK112 phosphorylation Cells were seeded into matrigel-coated 6-well plates at a density of 0.4 - 0.8 million cells per well 48 hours prior to experiment. When necessary, receptor induction was initiated on the same day with 6x10-1 IM mifepristone. 16 hours prior to experiment, cells were starved using serum-free growth media containing 1 % fatty acid-free bovine serum albumin (Sigma, St-Louis, MO). Cells were then stimulated with 2X agonist solutions in HBSS or Dulbelcco's phosphate buffered saline (D-PBS) (Invitrogen, Carlsbad, CA) for 5 minutes at 37°C. Following stimulation, cells were placed on ice and washed once with ice-cold buffer. Lysis buffer containing 150mM NaCl, 50mM TrisHEl pH 8., 0.25% sodium deoxycholate, 1 % igepal (NP-40), 2mM sodium orthovanadate, 1mM sodium fluoride, and protease inhibitors were then added and cells were scraped off the plates. Lysates were frozen immediately in liquid nitrogen and kept at -80°C until further analysis.

[00247] Lysate protein concentration was determined using the Bradford method (Amresco, Solon, OH). Cell lysate proteins (22 FLg/lane) were resolved by SDS-PAGE using 4-20% Tris-glycine gels (Invitrogen, Carlsbad, CA). Following electrophoresis, proteins were transferred to nitrocellulose membranes that were subsequently blocked with 5% fat-free milk in Tris-buffer saline containing 0.2% tween-20 (TBST). Membranes were immunoblotted with phospho-p44/42 MAPK monoclonal antibody (Cell Signaling Technology, Beverly,

MA) diluted 1:1000 in 5% milk/TBST overnight at 4°C. Secondary antibody was HRP-linked anti-mouse IgG diluted 1:2000 in 5% milk/TBST. Immunoreactive proteins were revealed using SuperSignal ECL solution (Pierce Chemical, Rockford, IL). Results were quantified using Kodak Image Station 440CF. In all experiments, we also assessed total amount of p44/42 MAPK loaded in each lane.

[00248] Membranes were stripped of phospho-specific antibodies using 0.2 M glycine pH 2.5 and re-blotted with p44/42 polyclonal antibodies (Cell Signaling Technology, Beverly, MA) diluted 1:1000 in 5% milk/TBST overnight at 4°C. Secondary antibody was HRP-linked anti-rabbit lgG diluted 1:2000 in 5% milk/TBST.

EXAMPLE 2

cAMP Experiments

[00249] cAMP content of cells was determined by a commercially-available chemiluminescent immunoassay kit (Applied Biosystems, Foster City, CA). Assay plates (96-well) were precoated with matrigel at a dilution of 1:400, and cells were seeded at a density of 60,000 cells/well (mT2R5), 75,000 cells/well (hT1R2/hT1R3) and 50,000 cells/well (hT1R1/R3) 48 hours prior to experiment. Induction of hT1R1/R3 expression was also initiated 48 hours prior to experiment. Cell media was aspirated and 90 µl of pre-warmed HBSS or D-PBS was added to each well. Cells were incubated for 45 minutes at 37°C, buffer was aspirated and 90 µl of pre-warmed agonist solutions in HBSS or D-PBS containing 50 µM rolipram and 0.7 to 5 µM forskolin was added to each of the corresponding wells. Plates were incubated for 15 minutes at 37°C. Agonists

were aspirated and stimulation was terminated with addition of 60 μl of lysis buffer into each well. cAMP levels were then determined as described by the kit instructions. An independent cAMP standard curve was performed on each 96-well plates used. Chemiluminescent signals were detected using a TopCount-NXT (PerkinElmer, Wellesley, MA) set at a read-time of 2 seconds/well.

EXAMPLE 3

Taste Study

[00250] A flavor acceptance study is conducted using a test composition comprising a T1R or T2R modulator identified according to the foregoing examples. A control composition lacking the T1R or T2R modulator, but which is otherwise substantially similar or identical to the test composition, is also used. The study employs a two-way crossover design, with all subjects evaluating both compositions, which are administered in one or more same amounts or doses. The test and control compositions are evaluated on a single study day. The sequence for administering the test and control compositions is randomized among subjects. All enrolled subjects complete all aspects of the study protocol. Subjects respond to each of the test and control compositions using ordinal taste scores (e.g., in the case of a putative T2R modulator 1 =very bitter, 2=bitter, 3=indifferent, 4=not that bitter, 5=not bitter at all). Adverse events are recorded. Effectiveness of a T1R or T2R modulator is determined by measuring a significant difference in palatability of the test composition when compared to the control composition.

RESULTS

[00251] The results of the MAP Kinase assays described *supra* demonstrate that the sweet and umami receptors activate ERK1/2 in a pertussis toxin sensitive fashion. The inventors used mT2R5, a mouse bitter receptor that recognizes cycloheximide **(80)** Chandrashekar et al. (2000), and the hT1R2/hT1R3 (hT1R2/R3) and hT1R1/hT1R3 (hT1R1/R3) combinations, the recently identified human receptors for sweet **(14, 15)** and MSG (umami) taste **(14, 15)** (Li et al (2002); Nelson et al (2002)) respectively. A clone stably expressing mT2R5 shows robust induction of ERK1/2 phosphorylation upon exposure to cycloheximide (**Figure 1A**). Activation of ERK1/2 by cycloheximide in mT2R5-expressing cells peaks at 3-5 minutes post-stimulation (**Figure 1B**). Other bitter substances including quinine and denatonium benzoate, sweeteners such as saccharin or sucrose and MSG do not induce ERK1/2 activation in mT2R5-expressing cells (**Figure 1A**). Similarly, stimulation of rT2R9, the rat receptor orthologue of mT2R5 **(85)** Bufe et al, *Nat. Genet.* 32(3): 397-401, with cycloheximide leads to ERK1/2 activation in transiently transfected HEK293 cells (**Figure 1C**). Sweeteners such as sucrose, saccharin, cyclamate and the sweet tasting amino acid D-tryptophan activate ERK1/2 in hT1R2/R3-expressing cells (**Figure 2A**). Here again, the effect is specific for sweeteners as bitter substances and MSG fail to activate ERK1/2 in hT1R2/R3-expressing cells (**Figure 2B**). MSG induces ERK1/2 activation in hT1R1/R3 expressing cells (**Figure 2B**). Sweeteners and bitter substances have no significant effect on the level of activated ERK1/2 in these cells (**Figure 2B**). The effects of cycloheximide on mT2R5, of saccharin, cyclamate, D-tryptophan and sucrose on

hT1R2/R3 and of MSG on hT1R1/R3 are receptor dependent since naive cells do not respond significantly to any of these modalities (**Figure 1E and Figure 2C** and results not shown).

[00252] Cycloheximide activates ERK1/2 in a dose-dependent fashion in mT2R5-expressing cells with an EC_{50} of 1.1 +/-0.4 μM (mean +/- SD of three independent determinations) (**Figure 1D**). Saccharin and sucrose also induce ERK1/2 activation in a dose-dependent fashion in hT1R2/R3-expressing cells (**Figure 3A and 3B**). As expected from taste thresholds (14) (Li et al (2002)), saccharin is much more potent with an EC_{50} of 277 +/- 47 RM compare to an EC_{50} of 73 +/- 37 mM for sucrose (mean +/- SD of three independent determinations) (**Figures 3A and 3B**). One of the hallmarks of umami taste is its spectacular enhancement by inosine monophosphate (IMP) **(86)** Yamaguchi et al, *Physiol. Behav.* 49(5): 833-841 (1991). Accordingly, in the ERK1/2 assay, we observe a leftward shift of MSG EC_{50} of about 30 folds in presence of 10 mM IMP (**Figure 3C**) (EC_{50} MSG: 6.7 +/- 3.4 mM, EC_{50} MSG in the presence of 10 MM IMP: 0.4 +/-0.3 mM; mean +/- SD of three independent determinations). PTX has been widely used as a powerful tool to discriminate among the different pathways used by GPCRs to activate ERK1/2 **(87)** Liebmann et al., *Cell Signal* 13(11): 833-41 (2001). Treatment of HEK293 cells with PTX prevents stimulation of ERK1/2 by cycloheximide (**Figure 2A**), by sucrose, saccharin, D-tryptophan and cyclamate (**Figure 2A**) and by MSG (**Figure 2B**) without affecting the response of epidermal growth factor (EGF), a known tyrosine kinase receptor agonist.

Collectively, these results indicate that taste receptors functionally couple to G; proteins to induce ERK1/2 activation in HEK293 cells.

[00253] Activation of bitter, sweet and umami receptors inhibit cAMP accumulation in HEK293 cells. Results described in **Figures 2 and 3** suggest that taste receptors should also functionally couple to an inhibition of adenylyl cyclase and a reduction of cAMP levels in HEK293 cells. **Figure 4A** shows that cycloheximide leads to a 70% reduction of forskolin-induced cAMP accumulation in mT2R5-expressing cells. In agreement with the involvement of G; proteins, PTX treatment fully abolishes the inhibition (**Figure 5A**). The effect of cycloheximide on cAMP accumulation is mT2R5-dependent since cAMP levels remain unchanged if the same experimental conditions are applied on naive HEK293 cells (**Figure 4A**). Cycloheximide inhibits cAMP accumulation in a dose-dependent fashion in mT2R5-expressing cells with an EC_{50} of 1.2 +/- 0.7 μM (**Figure 5A**) (mean +/- SD of three independent determinations) a value similar to the EC_{50} calculated for ERK1/2 activation (**Figure 5D**). The sweet taste hT1R2/R3 receptor also functionally couples to a robust inhibition of cAMP accumulation in HEK293 cells. Sweeteners such as aspartame, cyclamate, saccharin and monellin decrease forskolin-induced cAMP accumulation levels by 55%, 40%, 55% and 64% respectively and in a PTX-sensitive fashion (**Figure 5A**). Fructose and sucrose do not inhibit cAMP accumulation in hT1R2/R3-expressing cells, on the contrary; fructose apparently increase cAMP levels (**Figure 5A**). The lack of apparent effect of fructose and sucrose in the inhibition assay can be explained by the fact that these two sweeteners

consistently increase cAMP levels in HEK293 cells not expressing the sweet receptor (**Figure 5B**). Cyclamate (**Figure 5C**), aspartame (**Figure 5D**) and saccharin (**Figure 5E**) inhibit cAMP accumulation in a dose-dependent fashion with EC_{50}s of 1.2 +/- 0.7mM, 350 +/- 60 μM and 61 +/- 33 μM respectively (**Figure 5C**) (mean +/- SD of three independent determinations). Our hT1R1/hT1R3 umami taste receptor line exhibits a very high basal cAMP level relative to our mT2R5 and hT1R2/hT1R3 lines (mT2R5 line: 2.8 +/- 1.9 pmol/well, T2R2/R3 line: 4.5 +/- 1.9 pmol/well, hT1R1/hT1R3 line: 180 +/- 30 pmol/well). Under experimental conditions similar to the one used for the mT2R5 and hT1R2/hT1R3 lines (in the presence of forskolin), cAMP levels more than often reached non-linear range values with the hT1R1/hT1R3 line (results not shown). However, in the absence of forskolin, MSG decreases basal levels of cAMP by 50% in this cell line (**Figure 6**). On the other hand, cAMP levels remain unchanged even in the presence of MSG when receptor expression is not induced (**Figure 6**).

[00254] Sweet and bitter receptors do not couple to G_s-stimulation in HEK293 cells. Current models suggest that the sweet receptor may couple to GS to increase cAMP levels in TRCs **(9, 10)** (Gilbertson et al (2000); Margolskee (2002)). Clearly, our results with ERK1/2 activation and inhibition of cAMP accumulation point to a direct coupling to G_i proteins (**Figure 2, 3 and 5**). However, it is still possible that this receptor could have dual properties, coupling to both G_i and G_s. Therefore, we sought to determine if we could detect an agonist-induce increase in cAMP levels in the hT1R2/R3 sweet taste receptor

line. Under these experimental conditions (i.e. in the absence of forskolin), cAMP levels remain unchanged after stimulation with aspartame, cyclamate, saccharin and monellin (**Figure 7A**). On the other hand, a β-adrenergic receptor (β2AR) agonist, isoproterenol, induces a 100% increase of cAMP accumulation in hT1R2/hT1R3-expressing cells indicating that a functional receptor/G_s interection can be detected under these experimental conditions. The sweeteners do not induce an increase of CAMP levels even after inhibiting functional coupling to G_i With PTX (**Figure 7B**). On the other hand, the isoproterenol response increases significantly (by more than 17 fold) under these conditions, confirming that the β2AR couples to both G_i and G_s proteins in HEK293 cells **(88)** (Paaka et al, *Nature* 390:88-91 (1997). Our experiments with mT2R5 suggest that bitter receptors do not functionally couple to G_s either. Cycloheximide does not increase levels of cAMP in HEK293 cells, even after inhibiting coupling to G_i proteins with PTX (**Figure 7C**). Interestingly, inhibiting functional coupling to G_i with PTX in the umami taste hT1R1/hT1R3 line uncovers a modest increase of 25% in cAMP levels (**Figure 6**). Further experiments are necessary to determine if hT1R1/hT1R3 can indeed couple to G_s-signaling pathways in a significant fashion.

CONCLUSIONS

[00255] In this application, the present inventors have investigated the functional coupling of taste receptors to ERK1/2 activation and to the modulation of intracellular cAMP levels, two classical signaling events activated by dozens of GPCRs **(89, 90, 91)** (Morris et al., *Physiol. Rev.* 79(4): 1373-1430 (1999); Chin et

al., *Ann. NY Acad. Sci.* 968: 49-64 (2002); Liebmann et al, *J. Biol Chem.* 271(49): 31098-31105 (1996)). cAMP is a universal second messenger used by a plethora of cell surface receptors to relay signals from the extracellular milieu to the intracellular signaling machinery such as protein kinases, transcription factors and ion channels **(89, 90, 92)** (Morris and Malbon (1999); Chin et al (2002); Robinson-White and Stratakis, *Ann NY Acad. Sci.* 968: 256-270 (2002)). GPCRs activation of Gαs and $G\alpha_i$ respectively increase and decrease intracellular cAMP levels (Hanoune and Defer, *Annu Rev. Pharmacol. Toxical* 42: 145-174 (2001) **(39)**) (Hansom and Defr (2001)). The GTP-bound form of $G\alpha_s$ directly interacts and activates the 9 types of membrane-bound adenylyl cyclase (AC) known **(93)**. Conversely, the GTP-bound form of $G\alpha_i$ can directly interact and inhibit up to 6 different types of AC **(39)**. ERK1/2 is activated by G_q, G_s and Gi-coupled GPCRs (Liebmann et al (1996); Pierce et al., *Oncogene* 20(13): 1532-1539 (2001); Gutkind, J.S., *J. Biol Chem* 273(4): 1839-42 (1998) **(91, 94, 95)**) and, depending on the cellular context, several signaling pathways can be triggered to activate ERK1/2. Specifically, it is thought that G_i-coupled GPCRs activate ERK1/2 mainly via the free (activated) Gβγ subunits (Crespo et al. *Nature* 369: 418-20 (1994); Faure et al., *J. Biol Chem.* 269(11): 7852-7854 (1999) **(96, 97)**) that recruit and activate soluble tyrosine kinases of the Src (Gutkind, 1998 **(95)**) and Bruton families (Wan et al., *J. Biol Chem.* 272(27): 17209-15 (1997) **(98)**) or somehow transactivate receptor tyrosine kinases (RTKs) at the cell surface to initiate the cascade Liebmann et al. (2001); Wu et al. *Bioch. Biophys Acta.* 1582:100-106 (2002) **(87, 99)**).

[00256] We have shown that a rodent bitter receptor, mT2R5, the human sweet taste receptor, hT1R2/hT1R3, and the human umami taste receptor, hT1R1/R3, couples to the activation of ERK1/2 and the inhibition of cAMP accumulation in HEK293 cells. The bitter substance cycloheximide, the sweeteners saccharin, sucrose, cyclamate, D-tryptophan and the flavory amino acid MSG activate ERK1/2 exclusively in cells expressing their respective receptors. The effects of cycloheximide on mT2R5, saccharin and sucrose on hT1R2/R3 and MSG on hT1R1/R3 reach saturation at higher concentrations and their potency at activating ERK1/2 is similar to the ones reported for the G_{15}-induced calcium mobilization in HEK293 **(80, 14)** (Chandrashekar et al (2000); Li et al., (2002)). Similarly, cycloheximide, artificial sweeteners, a sweet protein as well as MSG decrease cAMP levels exclusively in cells expressing their respective taste receptors. Here again, the effects are receptor dependent and the potency of these compounds at inhibiting cAMP accumulation is in agreement with taste thresholds and EC_{50}'s reported for the $G_{\alpha 15}$-induced calcium mobilization in HEK293 (Chandrashekar (2000); Li et al. (2002); Temussi et al. *FEBS Lett.* 526(1-3): 1-4 (2002) **(80, 14, 100)**). Collectively, these results indicate that bitter compounds, sweeteners and MSG specifically activate their taste receptors to induce ERK1/2 activation and the reduction of cAMP accumulation in heterologous cells.

[00257] α-subunits of the G_i family including $G\alpha_{i1\text{-}1}$, $G\alpha_{i1\text{-}2}$, $G\alpha_{i1\text{-}3}$, $G\alpha_{i0\text{-}1}$, $G\alpha_{i0\text{-}2}$, α-transducin and α-gustducin contain a conserved carboxyl-terminal cystein residue that is a site for modification by PTX, a 5'-diphosphate-ribosyltransferase

isolated from *Bortadella* pertussis **(101)** (Fields et al. *Biochem J.* 321(P1-3): 561-71 (1997)). PTX specifically and irreversibly modifies these G-protein subunits in vivo with attachment of an ADP-ribose moiety and, as a result, this covalent modification physically uncouples the G-protein from activation by GPCRs **(101)** (Fields et al. (1997)). In our assays, incubation of cells with PTX abolishes the activation of ERK1/2 by the bitter, sweet and umami taste receptors indicating that one or more members of the G_i family functionally link the taste receptors to this signaling pathway in HEK293 cells. It is very likely that a-subunits of $G\alpha_{i1-3}$ subfamily are involved since expression of $G\alpha_{i1-2}$ is restricted to the brain (Offermanns, S. Naunyn Schmiedz Berg, *Arch Pharmacol.* 360(1): 5-13 (1999) **(102)**) and that α-transducin and α-gustducin expression is mostly restricted to the eye and the tongue (McLaughlin et al. (1994); Offermanns (1999) **(75, 102)**). Similarly, PTX prevents activation of ERK1/2 by other G_i-coupled GPCRs expressed in HEK293 cells or different cell lines (Della Rocca et al (1997); Della Rocca et al (1999); Soeder et al., *J. Biol Chem.* 274(17): 12017-12026 (1999); Alderton et al, *J. Biol Chem.*276(16): 13152-13460 (2001) – Alderton et al., *Br. J. Pharmacol.* 1341(1): 6-4 (2001) **(83, 84, 103-105)**). Every taste GPCR that we studied also couples to the inhibition of forskolin-induced cAMP accumulation in HEK293 cells and PTX-treatment totally abolishes the inhibition. This result clearly indicates that taste receptors directly couple to one or more member of the $G\alpha_{il-3}$ subfamily in these cells. In this signaling pathway, activated $G\alpha_i$ proteins directly interact and inhibit the membrane bound adenylyl cyclase. There is indeed no evidence yet for direct regulation of cAMP-

phosphodiesterases (PDEs) by the $G\alpha_{i1-3}$ subfamily or, in fact, by any member of the Gi family (Hanoune and Defer (2001) **(93)**).

[00258] It has been postulated that cyclic nucleotides such as cAMP and cGMP are involved in taste transduction (**10**, Margolskee (2002)). Denatonium benzoate and strychnine, two extremely bitter substances, were shown to decrease the level of cAMP and cGMP in mouse taste bud homogenates (Yan et al. (2001) **(76)**). In 1995, Margolskee and colleagues reported the purification of a transducin-activated PDE activity from TRCs (Ruiz-Avila et al (2001) **(28)**). These results have inspired a model in which bitter taste receptors couple to α-gustducin/α-transducin that in turn couples to the activation of a PDE in TRCs **(10)**. $G\alpha_i$ subunits are highly expressed in TRCs (McLaughlin et al. (1994); Katsukobe et al. (2000); Asano-Miyoshi (2000) **(75, 25, 26)**). We propose, as depicted schematically in **Figure 8**, that in addition to the hypothetical α-gustducin/α-transducin -PDE pathway, that bitter receptors may decrease intracellular levels of cAMP in TRCs through the direct inhibition of ACs by activated $G_{\alpha i5}$ (**Figure 8**). It is not yet clear what could be the role of cAMP in TRCs functions. A decrease of cAMP in TRCs has been proposed to activate a cyclic nucleotide monophosphate (cNMP)-suppressible channel, leading to depolarization (Kolesnikov and Margolskee, *Nature* 376:80-88 (1995) **(106)**). (10) A recent study (Zhang et al., (2003) **(18)**) showing the essential requirement of the PLCβ2 pathway for the detection of sweeteners, bitter compounds and amino acids in rodents suggest that the cAMP pathway plays only a minor role in taste perception, if any. Still, modulation of cAMP levels in TRCs could have other

effects than perception per se (**Figure 8**). A recent report suggests that adrenergic transmission within the taste bud could play a paracrine role in taste physiology (**29**, Harness et al. (2002)). In this scenario, cAMP could have more of a modulator role, controlling intensity and/or the duration of taste sensation. In addition, the cAMP response element-binding protein (CREB) and phosphorylated-CREB have been recently localized in TRCs **(55)**, suggesting that gene expression regulation can be potentially controlled, at least in part, by the level of cAMP in TRCs.

[00259] Over the past decade, three independent lines of observations had pointed to a potential role of cAMP in modulating sweet-taste signaling and sensation. First, early experiments showed that cAMP caused membrane depolarization of electrode-clamped mouse receptor cells (Tonosaki et al., *Nature* 331:304-6 (1988) **(107)**) and of patch-clamped frog receptor cells (Avanet et al, *Nature* 331:351-9 (1988)). Further investigation suggested that this depolarization could be mediated by a cAMP-dependent protein kinase inactivating an outward potassium current (Avanet et al (1988) **(108)**). Second, sweeteners and membrane permeant analogues of cAMP were shown to activate the same subset of hamster TRCs in vitro (Cummings and Kinnamon, *J. Neurophysiol.* 70(6): 2326-2336 (1993) **(109)**). In addition, just like cAMP (Avanet et al (1988) **(108)**), saccharin was shown to depolarize hamster and gerbil TRCs by reducing outward potassium currents (Cummings and Kinnamon, *J. Neurophysiol.* 75(3):1256-63 (1996); *Uchida and Sato, Chem. Senses.* 22(3): 163-164 (1997) **(110, 111)**). Lastly, sweeteners such as saccharin

and sucrose were shown to increase cAMP levels in rat taste epithelium (Striem et al., 1989 **(78)**), in mouse fungiform taste buds (Nakashima and Ninomiya, *Cell Physiol. Biochem.* 9(2):90-98 (1999) **(112)**) and in pig circumvallate papillae (**77**, Naim et al., 1991). Together, these observations have led to the suggestion that the sweet receptor couples to G_S in TRCs **(9, 10)**. In our hands, however, the sweet receptor clearly couples to a reduction of intracellular cAMP levels and activation of ERK1/2 through the direct functional coupling with G_i. Moreover, we have consistently failed in detecting a sweetener-induced accumulation of cAMP, even after inhibiting functional coupling of hT1R2/R3 to G_i proteins. It is noteworthy that we can detect a fructose or sucrose-induced cAMP accumulation in naive HEK293 cells. As mentioned above, we strongly suspect that this is a direct result of the osmotic shock triggered by the high concentrations of sucrose and fructose used in our experiments. Similarly, in an independent study, sucrose was shown to induce cAMP accumulation in tongue muscle membranes (Striem et al., (1989) **(78)**), a non-taste tissue. It is therefore possible that the sweeteners-induced increase in cAMP levels observed in rat taste epithelium (Striem et al (1989) **(78)**), in mouse fungiform taste buds (78) and in pig circumvallate papillae (Naim et al. (1991) **(77)**) occurs through a receptor-independent mechanism. In any case, our results do not support the hypothesis of a direct functional coupling of the sweet receptor to G_S (Gilbertson et al, 2000; Marlgokskee (2002) **(9, 10)**). The effect of MSG on the level of cyclic nucleotides in TRCs is much less understood. One report suggests that MSG induces a decrease in cAMP levels in circumvallate and foliate taste buds (Chaudhuri and Roper, *Ann NY Acad. Sci.* 855:398-406 (1998) **(113)**) while another report claims

an increase in cAMP levels in fungiform papillae (Ninomiya et al., *J. Nutr.* 130 (3S Suppl):9500-9530 (2001) **(114)**). Our data clearly demonstrates that the umami receptor functionally couples to a reduction of intracellular cAMP levels and to the G_i-induced activation of ERK1/2 in HEK293 cells. It is not known yet if the MSG (umami) receptor couples to α-gustducin in vivo. Our results point to $G\alpha_i$ as a strong candidate for its cognate G protein in TRCs (**Figure 8**).

[00260] These results suggest that gustducin is not the only Gα-subunit used for taste transduction. The level of co-expression in TRCs between T1R1 and T1R2 and α-gustducin is estimated at around -15% in rodents (Hoon et al., *Cell* 96(4): 541-551 (1999) **(115)**). Similarly, another study reported that only about 10% of T1R3 positive cells were also α-gustducin positive in mouse TRCs (Montmayeur et al., *Nat. Neurosci.* 4(5):492-498 (2001) **(116)**). Thus, in conclusion, most cells expressing the sweet and umami receptor subunits do not express α-gustducin. In consequence, one could expect that sweet and umami taste perception is mediated, in part, by a different G-protein. Perhaps the most compelling other evidence suggesting the involvement of other G-proteins is the residual responsiveness of α-gustducin deficient mice to bitter and sweet stimuli (Wang et al., (1996); He et al., (2002); Ruiz-Avila et al. (2001) **(17, 27, 28)**). A recent study shows that expression of a dominant negative form of α-gustducin, from the gustducin promoter in these deficient mice, further decreases the residual responsiveness to sweet and bitter stimuli, substantiating the notion on the involvement of another G protein (28, Ruiz-Avila et al., 2001). Independent studies report that umami **(117)** (Caicedo and Roper, *J. Physiol.* 544(pt 2): 501-

509 (2002), sweet **(117, 118)** (Caicedo and Roper (2002); Bernhardt et al., *J. Physiol.* 490(Pt. 2): 320-336 (1996)) and bitter (Caicedo and Roper, 2002; Caicedo and Roper, *Science* 291:1557-60 (2001); Akrabas et al., *Science*, 242:1047-1050 (1988) **(117, 119, 120)**) modalities trigger an increase of intracellular calcium concentration in TRCs. Moreover, bitter compounds lead to PTX-sensitive accumulation of inositol triphosphate in TRCs **(121, 122)**. These cells are enriched in classical G protein-signaling effectors such as phospholipase C-β2 (PLCβ2) **(18, 23, 26, 124)**, an enzyme known to be activated by the Gβγ subunit of G proteins belonging to the G_i family (20-24), the type-III inositol trisphosphate receptor (IP3R-III) **(123, 124)** and a transient receptor potential (trp) channel TRPM5 **(53, 72, 78)** (**Figure 8**). PLCβ2 and TRPM5 are essential for taste perception of sweeteners, bitter substances and amino acids in rodents **(18)**. Collectively, these observations suggest that the major taste transduction pathway in TRCs links α-gustducin to the activation of PLCβ2 and TRPM5, these events ultimately leading to membrane depolarization and taste perception (**Figure 8**) **(18)**. We propose that Gβγ subunits released from activated $G_{\alpha i}$ could also contribute to activation of PLCβ2 in TRCs (**Figure 8**). Herein, it was shown the mRNAs for PLβ32 and $G\alpha_{i\text{-}2}$ co-exist in the same TRCs and that $G\alpha_{i\text{-}2}$ - positive cells also express bitter taste receptors **(26)**. This pathway would directly complement the lack of α-gustducin in mice and would account for the residual responsiveness to bitter compounds and even possibly sweeteners. Confirmation of this signaling pathway can be evaluated in genetically engineered mice lacking α-gustducin in addition to one or more $G\alpha_i$ subunits.

Other Embodiments

[00261] Other embodiments will be evident to those of skill in the art. It should be understood that the foregoing detailed description is provided for clarity only and is merely exemplary. The spirit and scope of the present invention are not limited to the above examples, but are encompassed by the claims which follow.

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SEQUENCE LISTING

SEQ ID NO:1

Human T2R01 amino acid sequence

MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQL
FIFYVNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLKM
RISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLRKFFSQNATIQKEDTLAIQIFSFV
AEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRVPGRGAPISALLSILSFLILYFSH
CMIKVFLSSLKFHIRRFIFLFFILVIGIYPSGHSLILILGNPKLKQNAKKFLLHSKCCQ

SEQ ID NO:2

Human T2R01 nucleotide sequence

ATGCTAGAGTCTCACCTCATTATCTATTTTCTTCTTGCAGTGATACAATTTCTTCTTGGG
ATTTTCACAAATGGCATCATTGTGGTGGTGAATGGCATTGACTTGATCAAGCACAGAAAA
ATGGCTCCGCTGGATCTCCTTCTTTCTTGTCTGGCAGTTTCTAGAATTTTTCTGCAGTTG
TTCATCTTCTACGTTAATGTGATTGTTATCTTCTTCATAGAATTCATCATGTGTTCTGCG
AATTGTGCAATTCTCTTATTTATAAATGAATTGGAACTTTGGCTTGCCACATGGCTCGGC
GTTTTCTATTGTGCCAAGGTTGCCAGCGTCCGTCACCCACTCTTCATCTGGTTGAAGATG
AGGATATCCAAGCTGGTCCCATGGATGATCCTGGGGTCTCTGCTATATGTATCTATGATT
TGTGTTTTCCATAGCAAATATGCAGGGTTTATGGTCCCATACTTCCTAAGGAAATTTTTC
TCCCAAAATGCCACAATTCAAAAAGAAGATACACTGGCTATACAGATTTTCTCTTTTGTT
GCTGAGTTCTCAGTGCCATTGCTTATCTTCCTTTTTGCTGTTTTGCTCTTGATTTTCTCT
CTGGGGAGGCACACCCGGCAAATGAGAAACACAGTGGCCGGCAGCAGGGTTCCTGGCAGG
GGTGCACCCATCAGCGCGTTGCTGTCTATCCTGTCCTTCCTGATCCTCTACTTCTCCCAC
TGCATGATAAAAGTTTTTCTCTCTTCTCTAAAGTTTCACATCAGAAGGTTCATCTTTCTG
TTCTTCATCCTTGTGATTGGTATATACCCTTCTGGACACTCTCTCATCTTAATTTTAGGA
AATCCTAAATTGAAACAAAATGCAAAAAAGTTCCTCCTCCA**CAGTAAGTGCTGTCAGTGA**

SEQ ID NO:3

Human T2R02 amino acid sequence

MALSFSAILHIIMMSAEFFTGITVNGFLIIVNCNELIKHRKLMPIQILLMCIGMSRFGLQ
MVLMVQSFFSVFFPLLYVKIIYGAAMMFLWMFFSSISLWFATCLSVFYCLKISGFTQSCF
LWLKFRIPKLIPWLFWEAFWPL*ALHLCVEVDYAKNVEEDALRNTTLKKSKTKIKKISEV
LLVNLALIFPLAIFVMCTSMLLISLYKHTHRMQHGSHGFRNANTEAHINALKTVITFFCF
FISYFAAFMTNMTFSLPYRSHQFFMLKDIMAAYPSGHSVIIILSNSKFQQSFRRILCLKK
KL

SEQ ID NO:4

Human T2R02 nucleotide sequence

ATGGCCTTGTCTTTTTCAGCTATTCTTCATATTATCATGATGTCAGCAGAATTCTTCACA
GGGATCACAGTAAATGGATTTCTTATCATTGTTAACTGTAATGAATTGATCAAACATAGA
AAGCTAATGCCAATTCAAATCCTCTTAATGTGCATAGGGATGTCTAGATTTGGTCTGCAG
ATGGTGTTAATGGTACAAAGTTTTTTCTCTGTGTTCTTTCCACTCCTTTACGTCAAAATA
ATTTATGGTGCAGCAATGATGTTCCTTTGGATGTTTTTTAGCTCTATCAGCCTATGGTTT
GCCACTTGCCTTTCTGTATTTTACTGCCTCAAGATTTCAGGCTTCACTCAGTCCTGTTTT
CTTTGGTTGAAATTCAGGATCCCAAAGTTAATACCTTGGCTGCTTCTGGGAAGCGTTCTG
GCCTCTGTGAGCATTGCATCTGTGTGTCGAGGTAGATTACGCTAAAAATGTGGAAGAGGA
TGCCCTCAGAAACACCACACTAAAAAAGAGTAAAACAAAGATAAAGAAAATTAGTGAAGT
GCTTCTTGTCAACTTGGCATTAATATTTCCTCTAGCCATATTTGTGATGTGCACTTCTAT
GTTACTCATCTCTCTTTACAAGCACACTCATCGGATGCAACATGGATCTCATGGCTTTAG
AAATGCCAACACAGAAGCCCATATAAATGCATTAAAAACAGTGATAACATTCTTTTGCTT
CTTTATTTCTTATTTTGCTGCCTTCATGACAAATATGACATTTAGTTTACCTTACAGAAG
TCACCAGTTCTTTATGCTGAAGGACATAATGGCAGCATATCCCTCTGGCCACTCGGTTAT
AATAATCTTGAGTAATTCTAAGTTCCAACAATCATTTAGAAGAATTCTCTG**CCTCAAAAA**
GAAACTATGA

SEQ ID NO:5

Human T2R03 amino acid sequence

MMGLTEGVFLILSGTQFTLGILVNCFIELVNGSSWFKTKRMSLSDFIITTLALLRIILLC
IILTDSFLIEFSPNTHDSGIIMQIIDVSWTFTNHLSIWLATCLGVLYCLKIASFSHPTFL
WLKWRVSRVMVWMLLGALLLSCGSTASLINEFKLYSVFRGIEATRNVTEHFRKKRSEYYL
IHVLGTLWYLPPLIVSLASYSLLIFSLGRHTRQMLQNGTSSRDPTTEAHKRAIRIILSFF
FLFLLYFLAFLIASFGNFLPKTKMAKMIGEVMTMFYPAGHSFILILGNSKLKQTFVVMLR
CESGHLKPGSKGPIFS

SEQ ID NO:6

Human T2R03 nucleotide sequence

ATGATGGGACTCACCGAGGGGGTGTTCCTGATTCTGTCTGGCACTCAGTTCACACTGGGA
ATTCTGGTCAATTGTTTCATTGAGTTGGTCAATGGTAGCAGCTGGTTCAAGACCAAGAGA
ATGTCTTTGTCTGACTTCATCATCACCACCCTGGCACTCTTGAGGATCATTCTGCTGTGT
ATTATCTTGACTGATAGTTTTTTAATAGAATTCTCTCCCAACACACATGATTCAGGGATA
ATAATGCAAATTATTGATGTTTCCTGGACATTTACAAACCATCTGAGCATTTGGCTTGCC
ACCTGTCTTGGTGTCCTCTACTGCCTGAAAATCGCCAGTTTCTCTCACCCCACATTCCTC
TGGCTCAAGTGGAGAGTTTCTAGGGTGATGGTATGGATGCTGTTGGGTGCACTGCTCTTA
TCCTGTGGTAGTACCGCATCTCTGATCAATGAGTTTAAGCTCTATTCTGTCTTTAGGGGA
ATTGAGGCCACCAGGAATGTGACTGAACACTTCAGAAAGAAGAGGAGTGAGTATTATCTG
ATCCATGTTCTTGGGACTCTGTGGTACCTGCCTCCCTTAATTGTGTCCCTGGCCTCCTAC
TCTTTGCTCATCTTCTCCCTGGGGAGGCACACACGGCAGATGCTGCAAAATGGGACAAGC
TCCAGAGATCCAACCACTGAGGCCCACAAGAGGGCCATCAGAATCATCCTTTCCTTCTTC
TTTCTCTTCTTACTTTACTTTCTTGCTTTCTTAATTGCATCATTTGGTAATTTCCTACCA
AAAACCAAGATGGCTAAGATGATTGGCGAAGTAATGACAATGTTTTATCCTGCTGGCCAC
TCATTTATTCTCATTCTGGGGAACAGTAAGCTGAAGCAGACATTTGTAGTGATGCTCCGG
TGTGAGTCTGGTCATCTGAAGCCTGGATCCAA**GGGACCCATTTTCTCTTAG**

SEQ ID NO:7

Human T2R04 amino acid sequence

MLRLFYFSAIIASVILNFVGIIMNLFITVVNCKTWVKSHRISSSDRILFSLGITRFLMLG
LFLVNTIYFVSSNTERSVYLSAFFVLCFMFLDSSSVWFVTLLNILYCVKITNFQHSVFLL

LKRNISPKIPRLLLACVLISAFTTCLYITLSQASPFPELVTTRNNTSFNISEGILSLVVS
LVLSSSLQFIINVTSASLLIHSLRRHIQKMQKNATGFWNPQTEAHVGAMKLMVYFLILYI
PYSVATLVQYLPFYAGMDMGTKSICLIFATLYSPGHSVLIIITHPKLKTTAKKILCFKK

SEQ ID NO:8

Human T2R04 nucleotide sequence

ATGCTTCGGTTATTCTATTTCTCTGCTATTATTGCCTCAGTTATTTTAAATTTTGTAGGA
ATCATTATGAATCTGTTTATTACAGTGGTCAATTGCAAAACTTGGGTCAAAAGCCATAGA
ATCTCCTCTTCTGATAGGATTCTGTTCAGCCTGGGCATCACCAGGTTTCTTATGCTGGGA
CTATTTCTGGTGAACACCATCTACTTCGTCTCTTCAAATACGGAAAGGTCAGTCTACCTG
TCTGCTTTTTTTGTGTTGTGTTTCATGTTTTTGGACTCGAGCAGTGTCTGGTTTGTGACC
TTGCTCAATATCTTGTACTGTGTGAAGATTACTAACTTCCAACACTCAGTGTTTCTCCTG
CTGAAGCGGAATATCTCCCCAAAGATCCCCAGGCTGCTGCTGGCCTGTGTGCTGATTTCT
GCTTTCACCACTTGCCTGTACATCACGCTTAGCCAGGCATCACCTTTTCCTGAACTTGTG
ACTACGAGAAATAACACATCATTTAATATCAGTGAGGGCATCTTGTCTTTAGTGGTTTCT
TTGGTCTTGAGCTCATCTCTCCAGTTCATCATTAATGTGACTTCTGCTTCCTTGCTAATA
CACTCCTTGAGGAGACATATACAGAAGATGCAGAAAAATGCCACTGGTTTCTGGAATCCC
CAGACGGAAGCTCATGTAGGTGCTATGAAGCTGATGGTCTATTTCCTCATCCTCTACATT
CCATATTCAGTTGCTACCCTGGTCCAGTATCTCCCCTTTTATGCAGGGATGGATATGGGG
ACCAAATCCATTTGTCTGATTTTTGCCACCCTTTACTCTCCAGGACATTCTGTTCTCATT
ATTATCACACATCCTAAACTGAAAACAACAGCAAA**GAAGATTCTTTGTTTCAAAAAATAG**

SEQ ID NO:9

Human T2R05 amino acid sequence

MLSAGLGLLMLVAVVEFLIGLIGNGSLVVWSFREWIRKFNWSSYNLIILGLAGCRFLLQW
LIILDLSLFPLFQSSRWLRYLSIFWVLVSQASLWFATFLSVFYCKKITTFDRPAYLWLKQ
RAYNLSLWCLLGYFIINLLLTVQIGLTFYHPPQGNSSIRYPFESWQYLYAFQLNSGSYLP
LVVFLVSSGMLIVSLYTHHKKMKVHSAGRRDVRAKAHITALKSLGCFLLLHLVYIMASPF
SITSKTYPPDLTSVFIWETLMAAYPSLHSLILIMGIPRVKQTCQKILWKTVCARRCWGP

SEQ ID NO:10

Human T2R05 nucleotide sequence

ATGCTGAGCGCTGGCCTAGGACTGCTGATGCTGGTGGCAGTGGTTGAATTTCTCATCGGT
TTAATTGGAAATGGAAGCCTGGTGGTCTGGAGTTTTAGAGAATGGATCAGAAAATTCAAC
TGGTCCTCATATAACCTCATTATCCTGGGCCTGGCTGGCTGCCGATTTCTCCTGCAGTGG
CTGATCATTTTGGACTTAAGCTTGTTTCCACTTTTCCAGAGCAGCCGTTGGCTTCGCTAT
CTTAGTATCTTCTGGGTCCTGGTAAGCCAGGCCAGCTTATGGTTTGCCACCTTCCTCAGT
GTCTTCTATTGCAAGAAGATCACGACCTTCGATCGCCCGGCCTACTTGTGGCTGAAGCAG
AGGGCCTATAACCTGAGTCTCTGGTGCCTTCTGGGCTACTTTATAATCAATTTGTTACTT
ACAGTCCAAATTGGCTTAACATTCTATCATCCTCCCCAAGGAAACAGCAGCATTCGGTAT
CCCTTTGAAAGCTGGCAGTACCTGTATGCATTTCAGCTCAATTCAGGAAGTTATTTGCCT
TTAGTGGTGTTTCTTGTTTCCTCTGGGATGCTGATTGTCTCTTTGTATACACACCACAAG
AAGATGAAGGTCCATTCAGCTGGTAGGAGGGATGTCCGGGCCAAGGCTCACATCACTGCG
CTGAAGTCCTTGGGCTGCTTCCTCTTACTTCACCTGGTTTATATCATGGCCAGCCCCTTC
TCCATCACCTCCAAGACTTATCCTCCTGATCTCACCAGTGTCTTCATCTGGGAGACACTC
ATGGCAGCCTATCCTTCTCTTCATTCTCTCATATTGATCATGGGGATTCCTAGGGTGAAG
CAGACTTGTCAGAAGATCCTGTGGAAGACAGTGTGTGCTCG**GAGATGCTGGGGCCCATGA**

SEQ ID NO:11

Human T2R06 amino acid sequence

MLAAALGLLMPIAGAEFLIGLVGNGVPVVCSFRGWVKKM*GVPINSHDSGK*PLSPTQAD
HVGHKSVSTFPEQWLALLS*CLRVLVSQANM*FATFFSGFCCMEIMTFVXXXXXXXXXXX
XXXXXXXXXLLVSFKITFYFSALVGWTL*KPLTGNSNILHPILNLLFL*IAVQ*RRLIAI
CDVSVPLVFL*RHHRKMEDHTAVRRRLKPRXXXXXXXXXXXXXXXXLYMVSALARHFSMTF
*SPSDLTILAISATLMAVYTSFPSIVMVMRNQTCQRIL*EMICTWKS

SEQ ID NO:12

Human T2R06 nucleotide sequence

ATGTTGGCGGCTGCCCTAGGATTGCTGATGCCCATTGCAGGGGCTGAATTTCTCATTGGC
CTGGTTGGAAATGGAGTCCCTGTGGTCTGCAGTTTTAGAGGATGGGTCAAAAAAATGTAA
GGAGTCCCTATAAATTCTCATGATTCTGGTAAGTAGCCACTTTCTCCTACTCAGGCCGAT
CATGTTGGACATAAGTCTGTTTCCACTTTCCCAGAGCAGTGGTTGGCTTTACTATCTTAA
TGTCTTCGAGTCCTGGTAAGCCAGGCCAACATGTAGTTTGCCACTTTCTTCAGTGGCTTC
TGCTGCATGGAGATCATGACCTTTGTCCCGCTGACTTCTTGTAGCTGAAAAGACTGGGTT
TTTGTTTTTTGCTAGTGTCTTTCAAGATCACTTTTTATTTCTCAGCTCTTGTTGGCTGGA
CCCTTTAAAAACCCTTAACAGGAAACAGCAACATCCTGCATCCCATTTTAAATCTGTTAT
TTTTATAGATTGCTGTCCAGTGAAGGAGACTGATTGCTATTTGTGATGTTTCTGTTCCAC
TTGTCTTTTTGTAAAGACATCACAGGAAGATGGAGGACCACACAGCTGTCAGGAGGAGGC
TCAAACCAAGGTGCTCATCGCTCTGAACTTCCCCCTTTACATGGTTTCTGCCTTGGCCAG
ACACTTTTCCATGACCTTCTAATCTCCCTCTGATCTCACCATTCTTGCCATCTCTGCAAC
ACTCATGGCTGTTTATACTTCATTTCCGTCTATTGTAATGGTTATGAGGAATCAGACTTG
TCAGAGAATTCTGTAGGAGATGATATGTACATGGAAATCCTAG

SEQ ID NO:13

Human T2R07 amino acid sequence

MADKVQTTLLFLAVGEFSVGILGNAFIGLVNCMDWVKKRKIASIDLILTSLAISRICLLC
VILLDCFILVLYPDVYATGKEMRIIDFFWTLTNHLSIWFATCLSIYYFFKIGNFFHPLFL
WMKWRIDRVISWILLGCVVLSVFISLPATENLNADFRFCVKAKRKTNLTWSCRVNKTQHA
STKLFLNLATLLPFCVCLMSFFLLILSLRRHIRRMQLSATGCRDPSTEAHVRALKAVISF
LLLFIAYYLSFLIATSSYFMPETELAVIFGESIALIYPSSHSFILILGNNKLRHASLKVI
WKVMSILKGRKFQQHKQI

SEQ ID NO:14

Human T2R07 nucleotide sequence

ATGGCAGATAAAGTGCAGACTACTTTATTGTTCTTAGCAGTTGGAGAGTTTTCAGTGGGG
ATCTTAGGGAATGCATTCATTGGATTGGTAAACTGCATGGACTGGGTCAAGAAGAGGAAA
ATTGCCTCCATTGATTTAATCCTCACAAGTCTGGCCATATCCAGAATTTGTCTATTGTGC
GTAATACTATTAGATTGTTTTATATTGGTGCTATATCCAGATGTCTATGCCACTGGTAAA

GAAATGAGAATCATTGACTTCTTCTGGACACTAACCAATCATTTAAGTATCTGGTTTGCA
ACCTGCCTCAGCATTTACTATTTCTTCAAGATAGGTAATTTCTTTCACCCACTTTTCCTC
TGGATGAAGTGGAGAATTGACAGGGTGATTTCCTGGATTCTACTGGGGTGCGTGGTTCTC
TCTGTGTTTATTAGCCTTCCAGCCACTGAGAATTTGAACGCTGATTTCAGGTTTTGTGTG
AAGGCAAAGAGGAAAACAAACTTAACTTGGAGTTGCAGAGTAAATAAAACTCAACATGCT
TCTACCAAGTTATTTCTCAACCTGGCAACGCTGCTCCCCTTTTGTGTGTGCCTAATGTCC
TTTTTCCTCTTGATCCTCTCCCTGCGGAGACATATCAGGCGAATGCAGCTCAGTGCCACA
GGGTGCAGAGACCCCAGCACAGAAGCCCATGTGAGAGCCCTGAAAGCTGTCATTTCCTTC
CTTCTCCTCTTTATTGCCTACTATTTGTCCTTTCTCATTGCCACCTCCAGCTACTTTATG
CCAGAGACGGAATTAGCTGTGATTTTTGGTGAGTCCATAGCTCTAATCTACCCCTCAAGT
CATTCATTTATCCTAATACTGGGGAACAATAAATTAAGACATGCATCTCTAAAGGTGATT
TGGAAAGTAATGTCTATTCTAAAAGGAAGAAAATT**CCAACAACATAAACAAATCTGA**

SEQ ID NO:15

Human T2R08 amino acid sequence

MFSPADNIFIILITGEFILGILGNGYIALVNWIDWIKKKKISTVDYILTNLVIARICLIS
VMVVNGIVIVLNPDVYTKNKQQIVIFTFWTFANYLNMWITTCLNVFYFLKIASSSHPLFL
WLKWKIDMVVHWILLGCFAISLLVSLIAAIVLSCDYRFHAIAKHKRNITEMFHVSKIPYF
EPLTLFNLFAIVPFIVSLISFFLLVRSLWRHTKQIKLYATGSRDPSTEVHVRAIKTMTSF
IFFFFLYYISSILMTFSYLMTKYKLAVEFGEIAAILYPLGHSLILIVLNNKLRQTFVRML
TCRKIACMI

SEQ ID NO:16

Human T2R08 nucleotide sequence

ATGTTCAGTCCTGCAGATAACATCTTTATAATCCTAATAACTGGAGAATTCATACTAGGA
ATATTGGGGAATGGATACATTGCACTAGTCAACTGGATTGACTGGATTAAGAAGAAAAAG
ATTTCCACAGTTGACTACATCCTTACCAATTTAGTTATCGCCAGAATTTGTTTGATCAGT
GTAATGGTTGTAAATGGCATTGTAATAGTACTGAACCCAGATGTTTATACAAAAAATAAA
CAACAGATAGTCATTTTTACCTTCTGGACATTTGCCAACTACTTAAATATGTGGATTACC
ACCTGCCTTAATGTCTTCTATTTTCTGAAGATAGCCAGTTCCTCTCATCCACTTTTTCTC

TGGCTGAAGTGGAAAATTGATATGGTGGTGCACTGGATCCTGCTGGGATGCTTTGCCATT
TCCTTGTTGGTCAGCCTTATAGCAGCAATAGTACTGAGTTGTGATTATAGGTTTCATGCA
ATTGCCAAACATAAAAGAAACATTACTGAAATGTTCCATGTGAGTAAAATACCATACTTT
GAACCCTTGACTCTCTTTAACCTGTTTGCAATTGTCCCATTTATTGTGTCACTGATATCA
TTTTTCCTTTTAGTAAGATCTTTATGGAGACATACCAAGCAAATAAAACTCTATGCTACC
GGCAGTAGAGACCCCAGCACAGAAGTTCATGTGAGAGCCATTAAAACTATGACTTCATTT
ATCTTCTTTTTTTTCCTATACTATATTTCTTCTATTTTGATGACCTTTAGCTATCTTATG
ACAAAATACAAGTTAGCTGTGGAGTTTGGAGAGATTGCAGCAATTCTCTACCCCTTGGGT
CACTCACTTATTTTAATTGTTTTAAATAATAAACTGAGGCAGACATTTGTCAGAATGCTG
ACATGTA**GAAAAATTGCCTGCATGATATGA**

SEQ ID NO:17

Human T2R09 amino acid sequence

MPSAIEAIYIILIAGELTIGIWGNGFIVLVNCIDWLKRRDISLIDIILISLAISRICLLC
VISLDGFFMLLFPGTYGNSVLVSIVNVVWTFANNSSLWFTSCLSIFYLLKIANISHPFFF
WLKLKINKVMLAILLGSFLISLIISVPKNDDMWYHLFKVSHEENITWKFKVSKIPGTFKQ
LTLNLGVMVPFILCLISFFLLLFSLVRHTKQIRLHATGFRDPSTEAHMRAIKAVIIFLLL
LIVYYPVFLVMTSSALIPQGKLVLMIGDIVTVIFPSSHSFILIMGNSKLREAFLKMLRFV
KCFLRRRKPFVP

SEQ ID NO:18

Human T2R09 nucleotide sequence

ATGCCAAGTGCAATAGAGGCAATATATATTATTTTAATTGCTGGTGAATTGACCATAGGG
ATTTGGGGAAATGGATTCATTGTACTAGTTAACTGCATTGACTGGCTCAAAAGAAGAGAT
ATTTCCTTGATTGACATCATCCTGATCAGCTTGGCCATCTCCAGAATCTGTCTGCTGTGT
GTAATATCATTAGATGGCTTCTTTATGCTGCTCTTTCCAGGTACATATGGCAATAGCGTG
CTAGTAAGCATTGTGAATGTTGTCTGGACATTTGCCAATAATTCAAGTCTCTGGTTTACT
TCTTGCCTCAGTATCTTCTATTTACTCAAGATAGCCAATATATCGCACCCATTTTTCTTC
TGGCTGAAGCTAAAGATCAACAAGGTCATGCTTGCGATTCTTCTGGGGTCCTTTCTTATC
TCTTTAATTATTAGTGTTCCAAAGAATGATGATATGTGGTATCACCTTTTCAAAGTCAGT

CATGAAGAAAACATTACTTGGAAATTCAAAGTGAGTAAAATTCCAGGTACTTTCAAACAG
TTAACCCTGAACCTGGGGGTGATGGTTCCCTTTATCCTTTGCCTGATCTCATTTTTCTTG
TTACTTTTCTCCCTAGTTAGACACACCAAGCAGATTCGACTGCATGCTACAGGGTTCAGA
GACCCCAGTACAGAGGCCCACATGAGGGCCATAAAGGCAGTGATCATCTTTCTGCTCCTC
CTCATCGTGTACTACCCAGTCTTTCTTGTTATGACCTCTAGCGCTCTGATTCCTCAGGGA
AAATTAGTGTTGATGATTGGTGACATAGTAACTGTCATTTTCCCATCAAGCCATTCATTC
ATTCTAATTATGGGAAATAGCAAGTTGAGGGAAGCTTTTCTGAAGATGTTAAGATTTGTG
AAGTGTTTCCTTAGAAGAA**GAAAGCCTTTTGTTCCATAG**

SEQ ID NO:19

Human T2R10 amino acid sequence

MLRVVEGIFIFVVVSESVFGVLGNGFIGLVNCIDCAKNKLSTIGFILTGLAISRIFLIWI
IITDGFIQIFSPNIYASGNLIEYISYFWVIGNQSSMWFATSLSIFYFLKIANFSNYIFLW
LKSRTNMVLPFMIVFLLISSLLNFAYIAKILNDYKTKNDTVWDLNMYKSEYFIKQILLNL
GVIFFFTLSLITCIFLIISLWRHNRQMQSNVTGLRDSNTEAHVKAMKVLISFIILFILYF
IGMAIEISCFTVRENKLLLMFGMTTTAIYPWGHSFILILGNSKLKQASLRVLQQLKCCEK
RKNLRVT

SEQ ID NO:20

Human T2R10 nucleotide sequence

ATGCTACGTGTAGTGGAAGGCATCTTCATTTTTGTTGTAGTTAGTGAGTCAGTGTTTGGG
GTTTTGGGGAATGGATTTATTGGACTTGTAAACTGCATTGACTGTGCCAAGAATAAGTTA
TCTACGATTGGCTTTATTCTCACCGGCTTAGCTATTTCAAGAATTTTTCTGATATGGATA
ATAATTACAGATGGATTTATACAGATATTCTCTCCAAATATATATGCCTCCGGTAACCTA
ATTGAATATATTAGTTACTTTTGGGTAATTGGTAATCAATCAAGTATGTGGTTTGCCACC
AGCCTCAGCATCTTCTATTTCCTGAAGATAGCAAATTTTTCCAACTACATATTTCTCTGG
TTGAAGAGCAGAACAAATATGGTTCTTCCCTTCATGATAGTATTCTTACTTATTTCATCG
TTACTTAATTTTGCATACATTGCGAAGATTCTTAATGATTATAAAACGAAGAATGACACA
GTCTGGGATCTCAACATGTATAAAAGTGAATACTTTATTAAACAGATTTTGCTAAATCTG
GGAGTCATTTTCTTCTTTACACTATCCCTAATTACATGTATTTTTTTAATCATTTCCCTT

TGGAGACACAACAGGCAGATGCAATCGAATGTGACAGGATTGAGAGACTCCAACACAGAA
GCTCATGTGAAGGCAATGAAAGTTTTGATATCTTTCATCATCCTCTTTATCTTGTATTTT
ATAGGCATGGCCATAGAAATATCATGTTTTACTGTGCGAGAAAACAAACTGCTGCTTATG
TTTGGAATGACAACCACAGCCATCTATCCCTGGGGTCACTCATTTATCTTAATTCTAGGA
AACAGCAAGCTAAAGCAAGCCTCTTTGAGGGTACTGCAGCAATTGAAGTGCTGTGAGAAA
AG**GAAAAATCTCAGAGTCACATAG**

SEQ ID NO:21

Human T2R11 amino acid sequence

MANMLKNMLTMISAIDFIMGIQRSRVMVLVHCIDWIRRWKLSLIDFILTCWAISRIFXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXNHLCT*FATCLAVFYFLKIVNFSYLFYFWLK
WRINKVAFILPLVSAFSVYQLSFDVHF*CLLVSCPKKYERHMTGLLNVSNNKNVNNIIIF
FIGSLSSFSISSIFFLLLLLSS*RHMKHIRFNFRDCRTPVYGPISEPRKRFSFFVLLLYK
NLPFS

SEQ ID NO:22

Human T2R12 amino acid sequence

MSSIWETLFIRILVV*FIMGTVGN*FIVLVNIID*IRN*KVSLIDFILNCLAISRICFL*
ITILATSFNIGYEKMPDSKNLAVSFDILWTGSSYFCLSCTTCLSVFYFLKVANFSNPIFL
WMKWKIHKVLLFIVLEATISFCTTSILKEIIINSLI*ERVTIKGNLTFNYMDTMHDFTSL
FLLQMMFILPFVETLASILLLILSLWSHTRQMKLHGIYSRDPSTEAHVKPIKAIISFLLL
FIVHYFISIILTLACPLLDFVAARTFSSVLVFFHPSGHSFLLILRDSKLKQASLCVLKKM
KYAKKDIISHFYKHA

SEQ ID NO:23

Human T2R12 nucleotide sequence

ATGTCAAGCATTTGGGAGACACTGTTTATAAGAATTCTTGTAGTGTAATTCATAATGGGG
ACTGTGGGAAATTGATTCATTGTATTGGTTAATATCATTGACTGAATCAGGAACTGAAAG

GTCTCCCTGATTGATTTTATTCTCAACTGCTTGGCCATCTCCAGGATATGTTTCCTGTAG
ATAACAATTTTAGCTACCTCTTTCAATATAGGCTATGAGAAAATGCCTGATTCTAAGAAT
CTTGCAGTAAGTTTTGACATTCTCTGGACAGGATCCAGCTATTTCTGCCTGTCCTGTACC
ACTTGCCTCAGTGTCTTCTATTTCCTCAAGGTAGCCAACTTCTCCAATCCCATTTTCCTC
TGGATGAAATGGAAAATTCACAAGGTGCTTCTCTTTATTGTACTAGAGGCAACGATCTCT
TTCTGCACAACTTCCATTCTGAAGGAAATAATAATTAATAGTTTAATCTAAGAACGGGTA
ACAATAAAAGGCAACTTGACATTTAATTATATGGATACCATGCATGATTTCACTTCTCTG
TTTCTCCTTC**AG**ATGATGTTCATCCTTCCTTTTGTGGAAACACTGGCTTCCATTCTTCTC
TTAATCCTCTCCTTATGGAGCCACACCAGGCAGATGAAGCTACATGGTATTTATTCCAGG
GATCCCAGCACAGAAGCCCATGTAAAACCTATAAAAGCTATAATTTCATTTCTACTCCTC
TTTATTGTGCATTATTTCATCAGTATCATACTAACATTGGCCTGTCCTCTTCTAGACTTC
GTTGCGGCAAGGACTTTTAGTAGTGTGCTGGTATTTTTCCATCCATCTGGCCATTCATTT
CTTCTAATTTTACGGGACAGCAAACTGAAGCAAGCTTCTCTCTGTGTCCTGAAGAAGATG
AAGTATGCCAAAAAGGACATAATCT**CTCATTTTTATAAACATGCCTGA**

SEQ ID NO:24

Human T2R13 amino acid sequence

MESALPSIFTLVIIAEFIIGNLSNGFIVLINCIDWVSKRELSSVDKLLIILAISRIGLIW
EILVSWFLALHYLAIFVSGTGLRIMIFSWIVSNHFNLWLATIFSIFYLLKIASFSSPAFL
YLKWRVNKVILMILLGTLVFLFLNLIQINMHIKDWLDRYERNTTWNFSMSDFETFSVSVK
FTMTMFSLTPFTVAFISFLLLIFSLQKHLQKMQLNYKGHRDPRTKVHTNALKIVISFLLF
YASFFLCVLISWISELYQNTVIYMLCETIGVFSPSSHSFLLILGNAKLRQAFLLVAAKVW
AKR

SEQ ID NO:25

Human T2R13 nucleotide sequence

ATGGAAAGTGCCCTGCCGAGTATCTTCACTCTTGTAATAATTGCAGAATTCATAATTGGG
AATTTGAGCAATGGATTTATAGTACTGATCAACTGCATTGACTGGGTCAGTAAAAGAGAG
CTGTCCTCAGTCGATAAACTCCTCATTATCTTGGCAATCTCCAGAATTGGGCTGATCTGG
GAAATATTAGTAAGTTGGTTTTTAGCTCTGCATTATCTAGCCATATTTGTGTCTGGAACA

GGATTAAGAATTATGATTTTTAGCTGGATAGTTTCTAATCACTTCAATCTCTGGCTTGCT
ACAATCTTCAGCATCTTTTATTTGCTCAAAATAGCGAGTTTCTCTAGCCCTGCTTTTCTC
TATTTGAAGTGGAGAGTAAACAAAGTGATTCTGATGATACTGCTAGGAACCTTGGTCTTC
TTATTTTTAAATCTGATACAAATAAACATGCATATAAAAGACTGGCTGGACCGATATGAA
AGAAACACAACTTGGAATTTCAGTATGAGTGACTTTGAAACATTTTCAGTGTCGGTCAAA
TTCACTATGACTATGTTCAGTCTAACACCATTTACTGTGGCCTTCATCTCTTTTCTCCTG
TTAATTTTCTCCCTGCAGAAACATCTCCAGAAAATGCAACTCAATTACAAAGGACACAGA
GACCCCAGGACCAAGGTCCATACAAATGCCTTGAAAATTGTGATCTCATTCCTTTTATTC
TATGCTAGTTTCTTTCTATGTGTTCTCATATCATGGATTTCTGAGCTGTATCAGAACACA
GTGATCTACATGCTTTGTGAGACGATTGGAGTCTTCTCTCCTTCAAGCCACTCCTTTCTT
CTGATTCTAGGAAACGCTAAGTTAAGACAGGCCTTTCTTTTGGTGGCAGCTAA**GGTATGG**
GCTAAACGATGA

SEQ ID NO:26

Human T2R14 amino acid sequence

MGGVIKSIFTFVLIVEFIIGNLGNSFIALVNCIDWVKGRKISSVDRILTALAISRISLVW
LIFGSWCVSVFFPALFATEKMFRMLTNIWTVINHFSVWLATGLGTFYFLKIANFSNSIFL
YLKWRVKKVVLVLLLVTSVFLFLNIALINIHINASINGYRRNKTCSSDSSNFTRFSSLIV
LTSTVFIFIPFTLSLAMFLLLIFSMWKHRKKMQHTVKISGDASTKAHRGVKSVITFFLLY
AIFSLSFFISVWTSERLEENLIILSQVMGMAYPSCHSCVLILGNKKLRQASLSVLLWLRY
MFKDGEPSGHKEFRESS

SEQ ID NO:27

Human T2R14 nucleotide sequence

ATGGGTGGTGTCATAAAGAGCATATTTACATTCGTTTTAATTGTGGAATTTATAATTGGA
AATTTAGGAAATAGTTTCATAGCACTGGTGAACTGTATTGACTGGGTCAAGGGAAGAAAG
ATCTCTTCGGTTGATCGGATCCTCACTGCTTTGGCAATCTCTCGAATTAGCCTGGTTTGG
TTAATATTCGGAAGCTGGTGTGTGTCTGTGTTTTTCCCAGCTTTATTTGCCACTGAAAAA
ATGTTCAGAATGCTTACTAATATCTGGACAGTGATCAATCATTTTAGTGTCTGGTTAGCT
ACAGGCCTCGGTACTTTTTATTTTCTCAAGATAGCCAATTTTTCTAACTCTATTTTTCTC

TACCTAAAGTGGAGGGTTAAAAAGGTGGTTTTGGTGCTGCTTCTTGTGACTTCGGTCTTC
TTGTTTTTAAATATTGCACTGATAAACATCCATATAAATGCCAGTATCAATGGATACAGA
AGAAACAAGACTTGCAGTTCTGATTCAAGTAACTTTACACGATTTTCCAGTCTTATTGTA
TTAACCAGCACTGTGTTCATTTTCATACCCTTTACTTTGTCCCTGGCAATGTTTCTTCTC
CTCATCTTCTCCATGTGGAAACATCGCAAGAAGATGCAGCACACTGTCAAAATATCCGGA
GACGCCAGCACCAAAGCCCACAGAGGAGTTAAAAGTGTGATCACTTTCTTCCTACTCTAT
GCCATTTTCTCTCTGTCTTTTTTCATATCAGTTTGGACCTCTGAAAGGTTGGAGGAAAAT
CTAATTATTCTTTCCCAGGTGATGGGAATGGCTTATCCTTCATGTCACTCATGTGTTCTG
ATTCTTGGAAACAAGAAGCTGAGACAGGCCTCTCTGTCAGTGCTACTGTGGCTGAGGTAC
ATGTTCAAAGATGGGGAGCCCTCAGGTCACAAA**GAATTTAGAGAATCATCTTGA**

SEQ ID NO:28

Human T2R15 amino acid sequence

MITFLPIIFSILVVVTFVLGNFANGFIVLVNSIEWVKRQKISFADQILTALAVSRVGLLW
VILLHWYATVLNPGSYSLGVRITTINAWAVTNHFSIWVATSLSIFYFLKIANFSNFIFLH
LKRRIKSVIPVILLGSLLFLVCHLVVVNMDESMWTKEYEGNVSWEIKLSDPTHLSDMTVT
TLANLIPFTLSLLSFLLLICSLCKHLKKMQFHGKGSPDSNTKVHIKALQTVTSFLLLFAV
YFLSLITSIWNFRRRL*NEPVLMLSQTTAIIYPSFHSFILIWGSKKLKQTFLLILCQIKC

SEQ ID NO:29

Human T2R15 nucleotide sequence

ATGATAACTTTTCTACCCATCATTTTTTCCATTCTAGTAGTGGTTACATTTGTTCTTGGG
AATTTTGCTAATGGCTTCATAGTGTTGGTAAATTCCATTGAGTGGGTCAAGAGACAAAAG
ATCTCCTTTGCTGACCAAATTCTCACTGCTCTGGCAGTCTCCAGAGTTGGTTTGCTCTGG
GTAATATTATTACATTGGTATGCAACTGTTTTGAATCCAGGTTCATATAGTTTAGGAGTA
AGAATTACTACTATTAATGCCTGGGCTGTAACCAACCATTTCAGCATCTGGGTTGCTACT
AGCCTCAGCATATTTTATTTCCTCAAGATTGCCAATTTCTCCAACTTTATTTTTCTTCAC
TTAAAAAGGAGAATTAAGAGTGTCATTCCAGTGATACTATTGGGGTCTTTGTTATTTTTG
GTTTGTCATCTTGTTGTGGTAAACATGGATGAGAGTATGTGGACAAAAGAATATGAAGGA
AACGTGAGTTGGGAGATCAAATTGAGTGATCCGACGCACCTTTCAGATATGACTGTAACC

ACGCTTGCAAACTTAATACCCTTTACTCTGTCCCTGTTATCTTTTCTGCTCTTAATCTGT
TCTTTGTGTAAACATCTCAAGAAGATGCAGTTCCATGGCAAAGGATCTCCAGATTCCAAC
ACCAAGGTCCACATAAAAGCTTTGCAAACGGTGACCTCCTTCCTCTTGTTATTTGCTGTT
TACTTTCTGTCCCTAATCACATCGATTTGGAATTTTAGGAGGAGGCTGTAGAACGAACCT
GTCCTCATGCTCAGCCAAACTACTGCAATTATATACCCTTCATTTCATTCATTCATCCTA
ATTTGGGGAAGCAAGAAGCTGAAACAGACCTTTCTTTTGATTTT**GTGTCAGATTAAGTGC**
TGA

SEQ ID NO:30

Human T2R16 amino acid sequence

MIPIQLTVFFMIIYVLESLTIIVQSSLIVAVLGREWLQVRRLMPVDMILISLGISRFCLQ
WASMLNNFCSYFNLNYVLCNLTITWEFFNILTFWLNSLLTVFYCIKVSSFTHHIFLWLRW
RILRLFPWILLGSLMITCVTIIPSAIGNYIQIQLLTMEHLPRNSTVTDKLENFHQYQFQA
HTVALVIPFILFLASTIFLMASLTKQIQHHSTGHCNPSMKARFTALRSLAVLFIVFTSYF
LTILITIIGTLFDKRCWLWVWEAFVYAFILMHSTSLMLSSPTLKRILKGKC

SEQ ID NO:31

Human T2R16 nucleotide sequence

ATGATACCCATCCAACTCACTGTCTTCTTCATGATCATCTATGTGCTTGAGTCCTTGACA
ATTATTGTGCAGAGCAGCCTAATTGTTGCAGTGCTGGGCAGAGAATGGCTGCAAGTCAGA
AGGCTGATGCCTGTGGACATGATTCTCATCAGCCTGGGCATCTCTCGCTTCTGTCTACAG
TGGGCATCAATGCTGAACAATTTTTGCTCCTATTTTAATTTGAATTATGTACTTTGCAAC
TTAACAATCACCTGGGAATTTTTTAATATCCTTACATTCTGGTTAAACAGCTTGCTTACC
GTGTTCTACTGCATCAAGGTCTCTTCTTTCACCCATCACATCTTTCTCTGGCTGAGGTGG
AGAATTTTGAGGTTGTTTCCCTGGATATTACTGGGTTCTCTGATGATTACTTGTGTAACA
ATCATCCCTTCAGCTATTGGGAATTACATTCAAATTCAGTTACTCACCATGGAGCATCTA
CCAAGAAACAGCACTGTAACTGACAAACTTGAAAATTTTCATCAGTATCAGTTCCAGGCT
CATACAGTTGCATTGGTTATTCCTTTCATCCTGTTCCTGGCCTCCACCATCTTTCTCATG
GCATCACTGACCAAGCAGATACAACATCATAGCACTGGTCACTGCAATCCAAGCATGAAA
GCGCGCTTCACTGCCCTGAGGTCCCTTGCCGTCTTATTTATTGTGTTTACCTCTTACTTT

CTAACCATACTCATCACCATTATAGGTACTCTATTTGATAAGAGATGTTGGTTATGGGTC
TGGGAAGCTTTTGTCTATGCTTTCATCTTAATGCATTCCACTTCACTGATGCTGAGCAGC
CCTACGTTGAAAAG**GATTCTAAAGGGAAAGTGCTAG**

SEQ ID NO:32

Human T2R17 amino acid sequence

MCSAXLLIILSILVVFAFVLGNVANGFIALINVNDWVKTQKISSTDQIVTALAFSRIGLL
XTLIILLHWYATVFNSALYSLEVRIVPSNVSAIINHFSIWLATSLSIFYLFKIANFSNFI
FLHLKKRIKSVLLVILLGSLVFLICNLAVVTMDDSVWTKEFEGNVTWKIELRNAIHLSNM
TITNHASKLHTVHSDSNIFSAVSLFSXTMLANFTLFILTLISFLLLVCSPCKHLKMMQLH
GKGSQDLSTKVHIKPLQTVISFRMLFAIYFLCIITSTWNPRTQQSNLVFLLYQTLAIMYP
SFHSFILIMRSRKLKQTSLSVLCQVTCWVK

SEQ ID NO:33

Human T2R18 amino acid sequence

MFVGINIFFLVVATRGLVLGMLGNGLIGLVNCIEWAKSWKVSSADFILTSLAIVRIIRLY
LILFDSFIMVLSPHLYTIRKLVKLFTILWALINQLSI*FATCLSIFYLLKIANFSHSLFL
WLKWRMNGMIVMLLILSLFLLIFDSLVLEIFIDISLNIIDKSNLTLYLDESKTLYDKLSI
LKTLLSLTYVIPFLLTLTSLLLLFISLVRHTKNLQLNSLGSRDSSTEAHKRAMKMVIAFL
LLFIINFISTLIGDWIFLEVENYQVMMFIMMILLAFPSGHSFIIILGNNKLRQSSLRLLW
HLKFSLKKAKPLTS

SEQ ID NO:34

Human T2R18 nucleotide sequence

ATGTTCGTTGGAATTAATATTTTCTTTCTGGTGGTGGCAACAAGAGGACTTGTCTTAGGA
ATGCTGGGAAACGGGCTCATTGGACTGGTAAACTGCATTGAGTGGGCCAAGAGTTGGAAG
GTCTCATCAGCTGATTTCATCCTCACCAGCTTGGCTATAGTCAGAATCATTCGACTGTAT
TTAATACTATTTGATTCATTTATAATGGTATTGTCCCCTCATCTATATACCATCCGTAAA

CTAGTAAAACTGTTTACTATTCTTTGGGCATTAATTAATCAGTTAAGTATCTAGTTTGCC
ACCTGCCTAAGCATTTTCTACTTGCTTAAGATAGCCAATTTCTCCCACTCCCTTTTCCTC
TGGCTGAAGTGGAGAATGAACGGAATGATTGTTATGCTTCTTATATTGTCTTTGTTCTTA
CTGATTTTTGACAGTTTAGTGCTAGAAATATTTATTGATATCTCACTCAATATAATAGAT
AAAAGTAATCTGACTTTATATTTAGATGAAAGTAAAACTCTCTATGATAAACTCTCTATT
TTAAAAACTCTTCTCAGCTTGACATACGTTATTCCCTTTCTTCTGACTCTGACCTCTTTG
CTCCTTTTATTTATATCCTTAGTGAGACACACCAAGAATTTGCAGCTCAACTCTCTGGGC
TCAAGGGACTCCAGCACAGAGGCCCATAAAAGGGCCATGAAAATGGTGATAGCCTTCCTC
CTCCTTTTTATTATTAACTTTATTTCCACTTTAATAGGAGATTGGATCTTCCTTGAGGTA
GAGAATTATCAGGTCATGATGTTTATTATGATGATTTTACTTGCCTTTCCCTCAGGCCAC
TCATTTATTATAATTTTGGGAAACAACAAGCTAAGACAGAGCTCCTTGAGACTACTGTGG
CATCTTAAATTCTCTCTGAAAAAAGCAAAACCTTTAACTTCATAG

SEQ ID NO:35

Human T2R19 amino acid sequence

VTTLANLIPFTLSLICFLLLICSLCKHLKKMRLHSKGSQDPSTKVHIKALQTVTSFLMLF
AIYFLCIITSTWNLRTQQSKLVLLLCQTVAIMYPSFHSFILIMGSRKLKQTFLSVLWQMT
C

SEQ ID NO:36

Human T2R19 nucleotide sequence

CTGTAACTACTCTAGCAAACCTCATACCCTTTACTCTGAGCCTAATATGTTTTCTGCTGT
TAATCTGTTCTCTTTGTAAACATCTCAAGAAGATGCGGCTCCATAGCAAAGGATCTCAAG
ATCCCAGCACCAAGGTCCATATAAAAGCTTTGCAAACTGTGACCTCCTTCCTCATGTTAT
TTGCCATTTACTTTCTGTGTATAATCACATCAACTTGGAATCTTAGGACACAGCAGAGCA
AACTTGTACTCCTGCTTTGCCAAACTGTTGCAATCATGTATCCTTCATTCCACTCATTCA
TCCTGATTATGGGAAGTAGGAAGCTAAAACAGACCTTTCTTTCAGTTTTGTGGCAGATGA
CATGCTGAGTGAAAGAAGAGAAACCCTCAACTCCATAGATTCACAAGGGGAGCATCGTGG
GTCTTCTAGCAGAAAACAAACTGATGGTGTCTGGAACATTTTATAT

SEQ ID NO:37

Human T2R20 amino acid sequence

HLXRKAKSVVLVIVLGSLFFLVCQLVMKNTYINVWTEECEGNVTWKIKLRNAMHLSNLTV
AMLANLIPFTLTVISFLLLIYSLCKHLKKMQLHGKGSQDPSTKIHIKALQTVTSFLVLLA
IYFLCLIIS

SEQ ID NO:38

Human T2R20 nucleotide sequence

TTCATCACTTAN**AAAGGAAGGCTAAGAGTGTAG**TTCTGGTGATAGTGTTGGGGTCTTTGT
TCTTTTTGGTTTGTCAACTTGTGATGAAAAACACGTATATAAATGTGTGGACAGAAGAAT
GTGAAGGAAACGTAACTTGGAAGATCAAACTGAGGAATGCAATGCACCTTTCCAACTTGA
CTGTAGCCATGCTAGCAAACTTGATACCATTCACTCTGACCGTGATATCTTTTCTGCTGT
TAATCTACTCTCTGTGTAAACATCTGAAGAAGATGCAGCTCCATGGCAAAGGATCTCAAG
ATCCCAGCACCAAGATCCACATAAAAGCTCTGCAAACTGTGACCTCCTTCCTCGTATTAC
TTGCCATTTACTTTCT**GTGTCTAATCATATCCTTTTG**

SEQ ID NO:39

Human T2R21 amino acid sequence

MPPGIGNTFLIVMMGEFII*MLGNGFIVLVNCIDW*GVK*SY*TTASSPAWLSPQSVNFG
*YYLIHL*QHYGHIYMPSIN**NLFIFFGH*PIT*LPGLLP*CFLLL*NTYFSHPCFIWL
RWRISRTLLELPLGSLLLLFFNLALTGGLSDLWINIYTIYERNSTWSLDVSKILYCSLWI
LVSLIYLISFLLSLISLLLLILSLMRHIRNLQLNTMGPRDLRMKAHKRAMKMKMKMMVSF
LLFFLVHFSSLLPTGWIFLIQQK*QANFFVLLTSIIFPSSHSFVLILENCKLRQTAVGPL
WHLKCHLKRVKL

SEQ ID NO:40

Human T2R22 amino acid sequence

MATESDTNLLILAIAEFIISMLGNVFIGLVNCSEXIKNXKVFSADFILTCLAISHNGQLL
VILFDSFLVGLASHLYTTYRLXKNCIMLWT

SEQ ID NO:41

Human T2R22 nucleotide sequence

TATAGGGACN**GTGATGCTTCGTACACTCTC**CAAGAAGAAACACTCCGTGAGGTATGTGAG
ACTGCATNCCTTAGTAGATCTNTTGGGATATATATTCATAATATAGAAAAANAGGCAAAG
ACTTNCTTAAGTATATGAGACTCTATCCAACAGCAGAAGGTTCTGATCAAGACTGGAAGT
GCAATANAAGCAATGAAGATAAGTATCAGATATGAATGCTCTTCTGCAATGGTCTGATTG
TNACATTATTAATGATACANAGTATTAAAAACTTGGATTTTNTTGTCTCTGGAGATGGCC
ACCGAATCGGACACAAATCTTCTGATTCTGGCAATAGCAGAATTCATCATCAGCATGCTG
GGGAATGTGTTCATTGGACTGGTAAACTGCTCTGAANGGATCAAGAACCANAAGGTCTTC
TCAGCTGACTTCATCCTCACCTGCTTGGCTATCTCTCACAATGGACAACTGTTGGTGATA
CTGTTTGATTCATTTCTAGTGGGACTTGCTTCACATCTATATACCACATATAGACTANGA
AAAAACTGTATTATGCTTTGGACATGACTAATCACTTGACACACTGCTTCGCACGTGCTA
GCATATTCTATTCTTAGATAGCCACTTCNCACTCCTT**GTCTCTGCTGAAGTGGGAT**

SEQ ID NO:42

Human T2R23 amino acid sequence

VAFVLGNVANGFIALVNVIDXVNTRKISSAEQILTALVVSRIGXTLXHSIP*DATRC*SA
LYRXEVRIVASN

SEQ ID NO:43

Human T2R23 nucleotide sequence

AGGGTTGAGTCGTGCTTATCTTCACTTAACCTAGTATANAANTACAGCATATAGCAAGGA
GAGAATGTATATGAAGAGGAGTGAATTTGAGTCTGTTTGAGAATAATGACCTTTTCTATT
TCTATAAAGACAGTTTTGAATTCATCTATTAGCATATGCTGGTGCTTGCCTGTTGACACT

AGTCACTGAATTTAAAGGCAGAAAATGTTATTGCACATTTAGTAATCAAGTGTTCATCGA
AGTTAACATCTGGATGTTAAAGGACTCAGAACAAGTGTTACTAAGCCTGCATTTTTTTAT
CTGTTCAAACATGATGTGTTNTCTGCTCATCATTTCATCAATTCTGGTAGAGTTGCATTT
GTTCTTGGAAATGTNGCCAATGGCTTCATAGCTCTAGTAAATGTCATTGACTGNGTTAAC
ACACGAAAGATCTCCTCAGCTGAGCAAATTCTCACTGCTCTGGTGGTCTCCAGAATTGGT
NNTACTCTGNGTCATAGTATTCCTTGAGATGCAACTAGATGTTAATCTGCTCTATATAGG
NTAGAAGTAAGAATTGTTGCTTCTAATGCCTGAGCTCGTACGAACCATT

SEQ ID NO:44

Human T2R24 amino acid sequence

MATELDKIFLILAIAEFIISMLGNVFIGLVNCSEGIKNQKVFSADFILTCLAISTIGQLL
VILFDSFLVGLASHLYTTYRLGKTVIMLWHMTNHLTTWLATCLSIFYFFKIAHFPHSLFL
WLRWRMNGMIVMLLILSLFLLIFDSLVLEIFIDISLNIIDKSNLTLYLDESKTLYDKLSI
LKTLLSLTSFIPFSLFLTSLLFLFLSLVRHTRNLKLSSLGSRDSSTEAHRRAMKMVMSFL
FLFIVHFFSLQVANGIFFMLWNNKYIKFVMLALNAFPSCHSFILILGNSKLRQTAVRLLW
HLRNYTKTPNALPL

SEQ ID NO:45

Human T2R24 nucleotide sequence

ATGGCCACCGAATTGGACAAAATCTTTCTGATTCTGGCAATAGCAGAATTCATCATCAGC
ATGCTGGGGAATGTGTTCATTGGACTGGTAAACTGCTCTGAAGGGATCAAGAACCAAAAG
GTCTTCTCAGCTGACTTCATCCTCACCTGCTTGGCTATCTCCACAATTGGACAACTGTTG
GTGATACTGTTTGATTCATTTCTAGTGGGACTTGCTTCACATTTATATACCACATATAGA
CTAGGAAAAACTGTTATTATGCTTTGGCACATGACTAATCACTTGACAACCTGGCTTGCC
ACCTGCCTAAGCATTTTCTATTTCTTTAAGATAGCCCACTTCCCCCACTCCCTTTTCCTC
TGGCTGAGGTGGAGGATGAACGGAATGATTGTTATGCTTCTTATATTGTCTTTGTTCTTA
CTGATTTTTGACAGTTTAGTGCTAGAAATATTTATTGATATCTCACTCAATATAATAGAT
AAAAGTAATCTGACTTTATATTTAGATGAAAGTAAAACTCTCTATGATAAACTCTCTATT
TTAAAAACTCTTCTCAGCTTAACCAGTTTTATCCCCTTTTGTCTGTTCCTGACCTCCTTG
CTTTTTTTATTTCTGTCCTTGGTGAGACATACTAGAAATTTGAAGCTCAGTTCCTTGGGC

TCTAGAGACTCCAGCACAGAGGCCCATAGGAGGGCCATGAAAATGGTGATGTCTTTCCTT
TTCCTCTTCATAGTTCATTTTTTTTCCTTACAAGTGGCCAATGGGATATTTTTTATGTTG
TGGAACAACAAGTACATAAAGTTTGTCATGTTAGCCTTAAATGCCTTTCCCTCGTGCCAC
TCATTTATTCTCATTCTGGGAAACAGCAAGCTGCGACAGACAGCTGTGAGGCTACTGTGG
CATCTTAGGAACTATACAAAAACACCAAATGCTTTACCTTTGTAG

SEQ ID NO:46

Human T2R25 amino acid sequence

LSPFRMLFAIYFLCIITSTWNPRTQQSNLVFLLYQTLAIMYPSFHSFILIMRSRKLKQTS
LSVLCQVTCWVK

SEQ ID NO:47

Human T2R26 amino acid sequence

MPPGIGNTFLIVMMGEFII*MLGNGFIVLVNCIDVRSQMILLDNCILTSLAISTISQLWI
ILLDSFVTALWPHLYAFNKLIKFIHIFWALTNHLVTWLACCLSVFYFFKIAYFSHPCFIW
LRWRISRTLLELPLGSLLLLFFNLALTGGLSDLWINIYTMYERNSTWSLDVSKILYCSLW
ILVSLIYLISFLLSLISLLLLILSLMRHIRNLQLNTMGPRDLRMKAHKRAMKMKMKMMVS
FLLFFLVHFSSLLPTGWIFLIQQK

SEQ ID NO:48

Human T2R27 amino acid sequence

LANLIDWAENQICLMDFILSSLAICRTLLLGCCVAIRCTYNDYPNIDAVNHNLIKIITIF
DILRLVSK*LGIWFASYLSIFYLLKVALFHHAIFLWLKWRISRAVFTFLMIFLFFYISII
SMIKIKLFLDQC*YKI*EKLLLEGRCE*SPPSC*PDAH*PGVVYSLYHFSYLMFLVCYLP
KGKHCTAVVIGDWLQRPRTEAYVRAMNIMIAFFFHLLYSLGTSLSSVSYFLCKRKIVALG
AYLSYPLSHSFILIMENNKVRKAL

SEQ ID NO:49

Human T2R28 amino acid sequence

NICVLLIILSILVVSAFVLGNVANGFIALINVNDW

SEQ ID NO:50

Human T2R29 amino acid sequence

MQAALTAFFVLLFSLLSLLGIAANGFIVLVLGKEWL

SEQ ID NO:51

Human T2R30 amino acid sequence

MITFLPIIFSILVVVTFVLGNFSNGFIALVNSIEWVKTRKISSADQILTALVVSRVGLLW
VILLHWYANVFNSALYSSEVGAVASNISAIINHFSIWLATSLSIFYLLKIANFSNLIFLH
LKKRIRSVVLVILLGPLVFLICNLAVITMDDSVWTKEYEGNVTWKIKLRNAIHLSNMTVS
TLANLIPFILTLICFLLLICSLCKHLKKMQLHGKGSQDPSTKVHIKALQTVTSFLLLCAI
YFLSMIISVCNFGRLEKQPVFMFCQAIIFSYPSTHPFILILGNKKLKQIFLSVLRHVRYW
VKDRSLRLHRFTRGALCVF

SEQ ID NO:52

Human T2R30 nucleotide sequence

ATGATAACTTTTCTACCCATCATTTTTTCCATTCTGGTAGTGGTTACATTTGTTCTTGGA
AATTTTTCCAATGGCTTCATAGCTCTAGTAAATTCCATTGAGTGGGTCAAGACACGAAAG
ATCTCCTCAGCTGACCAAATCCTCACTGCTCTGGTGGTCTCCAGAGTTGGTTTACTCTGG
GTCATATTATTACATTGGTATGCAAATGTGTTTAATTCAGCTTTATATAGTTCAGAAGTA
GGAGCTGTTGCTTCTAATATCTCAGCAATAATCAACCATTTCAGCATCTGGCTTGCTACT
AGCCTCAGCATATTTTATTTGCTCAAGATTGCCAATTTCTCCAACCTTATTTTTCTCCAC
TTAAAGAAGAGAATTAGGAGTGTTGTTCTGGTGATACTGTTGGGTCCCTTGGTATTTTTG
ATTTGTAATCTTGCTGTGATAACCATGGATGACAGTGTGTGGACAAAAGAATATGAAGGA

AATGTGACTTGGAAGATCAAATTGAGGAATGCAATACACCTTTCAAATATGACTGTAAGC
ACACTAGCAAACCTCATACCCTTCATTCTGACCCTAATATGTTTTCTGCTGTTAATCTGT
TCTCTGTGTAAACATCTCAAGAAGATGCAGCTCCATGGCAAAGGATCTCAAGATCCCAGC
ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGACCTCCTTTCTTCTGTTATGTGCCATT
TACTTTCTGTCCATGATCATATCAGTTTGTAATTTTGGGAGGCTGGAAAAGCAACCTGTC
TTCATGTTCTGCCAAGCTATTATATTCAGCTATCCTTCAACCCACCCATTCATCCTGATT
TTGGGAAACAAGAAGCTAAAGCAGATTTTTCTTTCAGTTTTGCGGCATGTGAGGTACTGG
GTGAAAGACAGAAGCCTTCGTCTCCATAGATTCACAAGAGGGGCATTGTGTGTCTTCTAG

SEQ ID NO:53

Human T2R31 amino acid sequence

MTTFIPIIFSSVVVVLFVIGNFANGFIALVNSIERVKRQKISFADQILTALAVSRVGLLW
VLLLNWYSTVFNPAFYSVEVRTTAYNVWAVTGHFSNWLATSLSIFYLLKIANFSNLIFLH
LKRRVKSVILVMLLGPLLFLACQLFVINMKEIVRTKEFEGNMTWKIKLKSAMYFSXMTVT
IGAXLVPFTLSLISFLMLICSLCKHLKKMQLHGEGSQDLSTKVHIKALQTLISFLLLCAI
FFLFLIVSVWSPRRLRNDPVVMVSKAVGNIYLAFDSFILIWRTKKLKHTFLLILCQIRC

SEQ ID NO:54

Human T2R31 nucleotide sequence

ATGACAACTTTTATACCCATCATTTTTTCCAGTGTGGTAGTGGTTCTATTTGTTATTGGA
AATTTTGCTAATGGCTTCATAGCATTGGTAAATTCCATTGAGCGGGTCAAGAGACAAAAG
ATCTCTTTTGCTGACCAGATTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTTGCTCTGG
GTATTATTATTAAATTGGTATTCAACTGTGTTTAATCCAGCTTTTTATAGTGTAGAAGTA
AGAACTACTGCTTATAATGTCTGGGCAGTAACCGGCCATTTCAGCAACTGGCTTGCTACT
AGCCTCAGCATATTTTATTTGCTCAAGATTGCCAATTTCTCCAACCTTATTTTTCTTCAC
TTAAAGAGGAGAGTTAAGAGTGTCATTCTGGTGATGCTGTTGGGGCCTTTACTATTTTTG
GCTTGTCAACTTTTTGTGATAAACATGAAAGAGATTGTACGGACAAAAGAATTTGAAGGA
AACATGACTTGGAAGATCAAATTGAAGAGTGCAATGTACTTTTCANATATGACTGTAACC
ATTGGAGCANACTTAGTACCCTTTACTCTGTCCCTGATATCTTTTCTGATGCTAATCTGT
TCTCTGTGTAAACATCTCAAGAAGATGCAGCTCCATGGAGAAGGATCGCAAGATCTCAGC

ACCAAGGTCCACATAAAAGCTTTGCAAACTCTGATCTCCTTCCTCTTGTTATGTGCCATT
TTCTTTCTATTCCTAATCGTTTCGGTTTGGAGTCCTAGGAGGCTGCGGAATGACCCGGTT
GTCATGGTTAGCAAGGCTGTTGGAAACATATATCTTGCATTCGACTCATTCATCCTAATT
TGGAGAACCAAGAAGCTAAAACACACCTTTCTTTTGATTTTGTGTCAGATTAGGTGCTGA

SEQ ID NO:55

Human T2R32 amino acid sequence

HSFMLTMGSRKPKQTFLSAL

SEQ ID NO:56

Human T2R33 amino acid sequence

MVYFLPIIFSILVVFAFVLGNFSNGFIALVNVIDWVKRQKISSADQILTALVVSRVGLLW
VILLHWYANVFNSALYSLEVRIVASNISAVINHFSIWLAASLSIFYLLKIANFSNLIFLH
LKKRIKSVVLVILLGPLVFLICNLAVITMDERVWTKEYEGNVTWKIKLRNAIHLSSLTVT
TLANLIPFTLSLICFLLLICSLCKHLKKMQLHSKGSQDPSTKVHIKALQTVISFLMLCAI
YFLSIMISVWNLRSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFWQVRYW
VKGEKPSSP

SEQ ID NO:57

Human T2R33 nucleotide sequence

ATGGTATATTTTCTGCCCATCATTTTTTCCATTCTGGTAGTGTTTGCATTTGTTCTTGGA
AATTTTTCCAATGGCTTCATAGCTCTAGTAAATGTCATTGACTGGGTTAAGAGACAAAAG
ATCTCCTCAGCTGACCAAATTCTCACTGCTCTGGTGGTCTCCAGAGTTGGTTTACTCTGG
GTCATATTATTACATTGGTATGCAAATGTGTTTAATTCAGCTTTATATAGTTTAGAAGTA
AGAATTGTTGCTTCTAATATCTCAGCAGTAATCAACCATTTCAGCATCTGGCTTGCTGCT
AGCCTCAGCATATTTTATTTGCTCAAGATTGCCAATTTCTCCAACCTTATTTTTCTCCAC
CTAAAGAAGAGAATTAAGAGTGTTGTTCTGGTGATACTGTTGGGGCCCTTGGTATTTCTG
ATTTGTAATCTTGCTGTGATAACCATGGATGAGAGAGTGTGGACAAAAGAATATGAAGGA

AATGTGACTTGGAAGATCAAATTGAGGAATGCAATACACCTTTCAAGCTTGACTGTAACT
ACTCTAGCAAACCTCATACCCTTTACTCTGAGCCTAATATGTTTTCTGCTGTTAATCTGT
TCTCTTTGTAAACATCTCAAGAAGATGCAGCTCCATAGCAAAGGATCTCAAGATCCCAGC
ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCCTTCCTCATGTTATGTGCCATT
TACTTTCTGTCCATAATGATATCAGTTTGGAATCTTAGGAGTCTGGAAAACAAACCTGTC
TTCATGTTCTGCAAAGCTATTAGATTCAGCTATCCTTCAATCCACCCATTCATCCTGATT
TGGGGAAACAAGAAGCTAAAGCAGACTTTTCTTTCAGTTTTTTGGCAAGTGAGGTACTGG
GTGAAAGGAGAGAAGCCTTCATCTCCATAG

SEQ ID NO:58

Human T2R34 amino acid sequence

GSSRXKPPRIPHKKLCKLGPSFPHNNLPIYFLCXNHIVLEFLKMRPKKKCSLMLCQAFGI
IYPSFHSFILXWGNKTLKQTFLSVXWQVTCWAKGQNQSTP

SEQ ID NO:59

Human T2R35 amino acid sequence

NAIRPSKLWTVTEADKTSQPGTSANKIFSAGNLISHVNMSRRMQLHGKGSQHLSTRVHIK
AXQTVISFLMLXAIYFLCLITSTWNPRTQQSKLVFLLYQTLGFMYLLFHSFILTMGSRKP
KQTFLSAL

SEQ ID NO:60

Human T2R36 amino acid sequence

MICFLLIILSILVVFAFVLGNFSNGFIALVNVIDWVKRQKISSADQILTALVVSRVGLLW
VILLHWYSNVLNSALYSSEVIIFISNAWAIINHFSIWLATSLSIFYLLKIVNFSRLIFHH
LKRKAKSVVLVIVLGPLVFLVCHLVMKHTYINVWTKEYEGNVTWKIKLRNAIHLSNLTVS
TLANLIPFTLTLISFLLLIYSLCKHLKKMQLHGKGSQDPSTKVHIKALQTVTSFLLLCAI
YFLSMIISVCNFGRLEKQPVFMFCQAIIFSYPSTHPFILILGNKKLKQIFLSVFWQMRYW
VKGEKPSSP

SEQ ID NO:61

Human T2R36 nucleotide sequence

ATGATATGTTTTCTGCTCATCATTTTATCAATTCTGGTAGTGTTTGCATTTGTTCTTGGA
AATTTTTCCAATGGCTTCATAGCTCTAGTAAATGTCATTGACTGGGTCAAGAGACAAAAG
ATCTCCTCAGCTGACCAAATCCTCACTGCTCTGGTGGTCTCCAGAGTTGGTTTACTCTGG
GTAATATTATTACATTGGTATTCAAATGTGTTGAATTCAGCTTTATATAGTTCAGAAGTA
ATAATTTTTATTTCTAATGCCTGGGCAATAATCAACCATTTCAGCATCTGGCTTGCTACT
AGCCTCAGCATATTTTATTTGCTCAAGATCGTCAATTTCTCCAGACTTATTTTTCATCAC
TTAAAAAGGAAGGCTAAGAGTGTAGTTCTGGTGATAGTGTTGGGTCCCTTGGTATTTTTG
GTTTGTCACCTTGTGATGAAACACACGTATATAAATGTGTGGACAAAAGAATATGAAGGA
AATGTGACTTGGAAGATCAAACTGAGGAATGCAATACACCTTTCAAACTTGACTGTAAGC
ACACTAGCAAACTTGATACCCTTCACTCTGACCCTGATATCTTTTCTGCTGTTAATCTAC
TCTCTGTGTAAACATCTCAAGAAGATGCAGCTCCATGGCAAAGGATCTCAAGATCCCAGC
ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGACCTCCTTTCTTCTGTTATGTGCCATT
TACTTTCTGTCCATGATCATATCAGTTTGTAATTTTGGGAGGCTGGAAAAGCAACCTGTC
TTCATGTTCTGCCAAGCTATTATATTCAGCTATCCTTCAACCCACCCATTCATCCTGATT
TTGGGAAACAAGAAGCTAAAGCAGATTTTTCTTTCAGTTTTTTGGCAAATGAGGTACTGG
GTGAAAGGAGAGAAGCCTTCATCTCCATAG

SEQ ID NO:62

Human T2R37 amino acid sequence

MITFLPIIFSILIVVTFVIGNFANGFIALVNSIEWVKRQKISSADQISHCSGGVQNWFTL
GHIITLVCNCV*FGFI*IRSKNFWF*CLSNNQAFQHVGVTSLSIFHLLKTANFSNLIFLH
LKKRIKSVGLVILLGPLLFFICNLFVINMDESVWTKEYEGNVTWKIKLRSAMYHSNMTLT
MLANFVPFTLTLISFLLLICSLCKHLKKMQLHGKGSQDPSTKVHIKALQTVTSFLLLCAI
YFLSMIISVCNLGRLEKQPVFMFCEAIIFSYPSTHPFILILGNKKLKQIFLSVLRHVRYW
VKGEKPSSS

SEQ ID NO:63

Human T2R37 nucleotide sequence

ATGATAACTTTTCTGCCCATCATTTTTTCCATTCTAATAGTGGTTACATTTGTGATTGGA
AATTTTGCTAATGGCTTCATAGCTCTAGTAAATTCCATTGAGTGGGTTAAGAGACAAAAG
ATCTCATCAGCTGACCAAATTTCTCACTGCTCTGGTGGTGTCCAGAATTGGTTTACTCTG
GGTCATATTATTACATTGGTATGCAACTGTGTTTAATTTGGCTTCATATAGATTAGAAGT
AAGAATTTTTGGTTCTAATGTCTCAGCAATAACCAAGCATTTCAGCATGTGGGTGTTACT
AGCCTCAGCATATTTCATTTGCTCAAGACTGCCAATTTCTCCAACCTTATTTTTCTCCAC
CTAAAGAAGAGGATTAAGAGTGTTGGTTTGGTGATACTATTGGGGCCTTTGCTATTTTTC
ATTTGTAATCTTTTTGTGATAAACATGGATGAGAGTGTATGGACAAAAGAATATGAAGGA
AACGTGACTTGGAAGATCAAATTGAGGAGTGCAATGTACCATTCAAATATGACTCTAACC
ATGCTAGCAAACTTTGTACCCTTCACTCTGACCCTGATATCTTTTCTGCTGTTAATCTGT
TCTCTGTGTAAACATCTCAAGAAGATGCAGCTCCATGGCAAAGGATCTCAAGATCCCAGC
ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGACCTCCTTTCTTCTGTTATGTGCCATT
TACTTTCTGTCCATGATCATATCAGTTTGTAATTTGGGGAGGCTGGAAAAGCAACCTGTC
TTCATGTTCTGCGAAGCTATTATATTCAGCTATCCTTCAACCCACCCATTCATCCTGATT
TTGGGAAACAAGAAGCTAAAGCAGATTTTTCTTTCAGTTTTGCGGCATGTGAGGTACTGG
GTGAAAGGAGAGAAGCCTTCATCTTCATAG

SEQ ID NO:64

Human T2R38 amino acid sequence

MLTLTRIRTVSYEVRSTFLFISVLEFAVGFLTNAFVFLVNFWDVVKRQPLSNSDCVLLCL
SISRLFLHGLLFLSAIQLTHFQKLSEPLNHSYQAIIMLWMIANQANLWLAACLSLLYCSK
LIRFSHTFLICLASWSPGRSPVPS

SEQ ID NO:65

Human T2R39 amino acid sequence

LRNAGLNDSNAKLVRNNDLLLINLILLLPLSVFVMCTSMLFVSLYKHMHWMQSESHKLSS
ARTEAHINALKTVTTFFCFFVSYFAAFMANMTFRIPYRSHQFFVVKEIMAAYPAGHSVII
VLSNSKFKDLFRRMICLQKE

SEQ ID NO:66

Human T2R40 amino acid sequence

SQYSLGHSYVVIFGYGQMKKTFLGILWHLKCGLKGRALLATQVGLREKSTRSLGVIFLAS
SYSFFVYVLCH

SEQ ID NO:67

Human T2R41 amino acid sequence

MITFLLIILSILVVFAFVLGNFSNGFIALVNVIDWVNTRKISSADQILTALAVSRVGLLW
VILLHWYANVLNPALYSSEVIIFISNISAIINHFSIWLATSLSIFYLLKIVNFSRLIFHH
LKRKAKSVVLVIVLGPLVFLVCHLVMKHTYINVWTKEYEGNVTWKIKLRNAIHLSNLTVS
TLANLIPFTLTLISFLLLICSLCKHLKKMQLHSKGSQDPSTKVHIKALQTVTSFLMLFAI
YFLYLITSTWNL*TQQSKLVFMFCQTLGIMYPSFHSFILIMGSRKLKQTFLSVLCQVTCL
VKGQQPSTP

SEQ ID NO:68

Human T2R42 amino acid sequence

FIGLTDCIAWMRNQKLCMVGFILTRMALARINIL

SEQ ID NO:69

Human T2R43 amino acid sequence

LELIFS*KVVATRGLVLGMLGNGLIGLVNCIEWAKSWKVSSADFILTSLAIVRIIRLYLI
LFDSFIMVLSPHLYTXXXXXXXXXXXXXXXXXXXXXXXXSLSIFHWFKTANFSNLIFLPLK

EED*NVWLGDAVGALGIFHL*SCSENHG*EVCGQKNMKEFCSGMIKLRNAIQLSNLTVTM
PANVTPCTLTLISFLLLIYSPCKHVKKMQLHGKGSQHLSTKVHIKVLQTVISFFLLCAIY
FVSVIISVWSFKNLENKPVFMFCQAIGFSCSSAHPFILTMGNKKLKQTYLSVLWQMR

SEQ ID NO:70

Human T2R44 amino acid sequence

MITFLPIIFSILIVVIFVIGNFANGFIALVNSIEWVKRQKISFVDQILTALAVSRVGLLW
VLLLHWYATQLNPAFYSVEVRITAYNVWAVTNHFSSWLATSLSMFYLLRIANFSNLIFLR
IKRRVKSVVLVILLGPLLFLVCHLFVINMDETVWTKEYEGNVTWKIKLRSAMYHSNMTLT
MLANFVPLTLTLISFLLLICSLCKHLKKMQLHGKGSQDPSTKVHIKALQTVTSFLLLCAI
YFLSMIISVCNLGRLEKQPVFMFCQAIIFSYPSTHPFILILGNKKLKQIFLSVLRHVRYW
VKDRSLRLHRFTRGALCVF

SEQ ID NO:71

Human T2R45 amino acid sequence

MATELDKIFLILAIAEFIISMLGNVFIGLVNCSEGIKNQKVFSADFILTCLAISTIGQLL
VILFDSFLVGLASHLYTTYRLGKTVIMLWHMTNHLTTWLATCLSIFYFFKIAHFPHSLFL
WLRWRMNGMIVMLLILSLFLLIFDSLVLEIFIDISLNIIDKSNLTLYLDESKTLYDKLSI
LKTLLSLTSFIPFSLFLTSLLFLFLSLVRHTRNLKLSSLGSRDSSTEAHRRAMKMVMSFL
FLFIVHFFSLQVANWIFFMLWNNKCIKFVMLALNAFPSCHSFILILGNSKLQQTAVRLLW
HLRNYTKTPNPLPL

SEQ ID NO:72

Human T2R46 amino acid sequence

MSFLHIVFSILVVVAFILGNFANGFIALINFIAWVKKQKISSADQIIADKQSPELVCSG

SEQ ID NO:73

Human T2R47 amino acid sequence

MLNALYSILIIIINI*FLIGILGNGFITLVNGIDWVKM*KRSSILTALTISRICLISVIM
VRWFI

SEQ ID NO:74

Human T2R48 amino acid sequence

VSRVGLLWVILLHWYSTVLNPTSSNLKVIIFISNAWAVTNHFSIWLATSLSIFYLLKIVN

SEQ ID NO:75

Human T2R49 amino acid sequence

TVTMLANLVPFTVTLISFLLLVCSLCKHLKKMHLHGKGSQDPSTKVHIKVLQTVISFLLL
CAIYFVSVIISS

SEQ ID NO:76

Human T2R50 amino acid sequence

MITFLPIIFSILVVVTFVIGNFANGFIALVNSTEWVKRQKISFADQIVTALAVSRVGLLW
VLLLNWYSTVLNPAFYSVELRTTAYNIWAVTGHFSNWPATSLSIFYLLKIANFSNLIFLR
LKRRVKSVILVVLLGPLLFLACHLFVVNMNQIVWTKEYEGNMTWKIKLRRAMYLSDTTVT
MLANLVPFTVTLISFLLLVCSLCKHLKKMQLHGKGSQDPSTKVHIKVLQTVISFFLLCAI
YFVSVIISVWSFKNLENKPVFMFCQAIGFSCSSAHPFILIWGNKKLKQTYLSVLWQMRY

SEQ ID NO:77

Rat T2R01 amino acid sequence

MMEGHILFFFLVVMVQFVTGVLANGLIVVVHAIDLIMWKKMAPLDLLLFCLATSRIILQL
CILFAQLCLFSLVRHTLFEDNITFVFIINELSLWFATWLGVFYCAKIATIPHPLFLWLKM

RISRLVPWLILGSVLYVIITTFIHSRETSAILKPIFISLFPKNATQVGTGHATLLSVLVL
GLTLPLFIFTVAVLLLIYSLWNYSRQMRTMVGTREYSGHAHISAMLSILSFLILYLSHYM
VAVLISTQVLYLGSRTFVFCLLVIGMYPSIHSIVLILGNPKLKRNAKMFIVHCKCCHCTR
AWVTSRSPRLSDLPVPPTHPSANKTSCSEACIMPS

SEQ ID NO:78

Rat T2R01 nucleotide sequence

CAGGAATCATAAATGGCTGAAACTGGGCAGAACTCTATGCATTATTTAAAGAAGTCATTG
GTTTGTCATTCTTAAA**ATGATGGAAGGGCATATACTCTTCTTCTTTTTGGTTGTGATGGT**
GCAGTTTGTCACTGGGGTCTTGGCAAATGGCCTCATTGTGGTTGTCCATGCTATTGACTT
GATCATGTGGAAGAAAATGGCCCCGTTGGATCTGCTTCTATTTTGCCTGGCGACTTCTCG
GATCATTCTGCAGTTATGTATATTGTTTGCACAATTGTGTCTATTCTCTTTGGTGAGACA
CACTTTATTTGAGGACAATATTACCTTTGTCTTCATCATAAATGAACTGAGTCTTTGGTT
TGCTACATGGCTCGGTGTTTTCTACTGTGCCAAGATTGCTACCATTCCTCACCCACTCTT
TCTGTGGCTGAAGATGAGGATATCCAGGTTGGTACCATGGCTGATCCTGGGATCTGTGCT
CTATGTAATTATTACTACTTTCATCCATAGCAGAGAGACTTCAGCAATCCTTAAACCAAT
TTTTATAAGCCTTTTTCCTAAAAATGCAACTCAAGTCGGAACAGGGCATGCCACACTACT
CTCAGTCCTGGTCCTTGGGCTCACACTGCCGTTGTTCATCTTTACTGTTGCTGTTCTGCT
CTTGATATACTCCCTGTGGAATTATAGCAGGCAGATGAGGACTATGGTAGGCACCAGGGA
GTATAGCGGACATGCTCACATCAGTGCAATGCTGTCCATTCTATCATTCCTCATCCTCTA
TCTCTCCCACTACATGGTGGCTGTTCTGATCTCTACTCAAGTCCTCTACCTTGGAAGCAG
AACCTTTGTATTCTGCTTACTGGTTATTGGTATGTACCCCTCAATACACTCGATTGTCTT
AATTTTAGGAAATCCTAAGCTGAAACGAAATGCAAAAATGTTCATTGTCCATTGTAAGTG
TTGTCATTGTACAAGAGCTTGGGTCACCTCAAGGAGCCCAAGACTCAGTGACTTGCCAGT
GCCTCCTACTCATCCCTCAGCCAACAAGACATCCTGCTCAGAAGCCTGTATAATGCCATC
CTAATTGTCCAGCCTGAGGTTTAATCCTAGGTTTGGTACTATTTCAAAGAGTAAAGTTGA
TCATTAAAGCACAACATATGTTGGTGGATGACATCAAGGTCCATATCCCAGTTGTCAATT
GTAAACCTCACCTTGCAAGATGATGTCACTGAGAAAGCAGGACAAATGGAGTCTAGGTCC
TTCTGTATGACTTGCTGCAGTATATGTGAATCTATAATTTTCTCCAAAAAAACAAAAAAA
AAAAAAAAAAA

SEQ ID NO:79

Rat T2R02 amino acid sequence

MFSQKTNYSHLFTFSIIFYVEIVTGILGNGFIALVNIMDWLKRRRISTADQILTALALTR
LIYVWSVLICILLLFLCPHLSMRPEMFTAIGVIWVVDNHFSIWLATCLGVFYFLKIASFS
NSLFLYLKWRVKKVVLMIILISLIFLMLNISSLGMYDHFSIDVYEGNMSYNLVDSTHFPR
IFLFTNSSKVFLIANSSHVFLPINSLFMLIPFTVSLVAFFVLFLSLWKHHKKMQVNAKGP
RDASTMAHTKALQIGFSFLLLYAIYLLFIITGILNLDLMRCIVILLFDHISGAVFSISHS
FVLILGNSKLRQATLSVLPCLRCRSKDMDTVVF

SEQ ID NO:80

Rat T2R02 nucleotide sequence

ATTTTGCTCCACTATTTTGCTCTTCTGCAGTAACACAGACCACAAAACAATGGAGCCAAT
GGGTCAAGAGCTGAAACTTCAGGAAGTGGGAGCCAAATTTTCTTTGTGATAGGTTGGCAT
ATGAGAATTCATTATTTGATGCAGCTTCTGAAAACTGGATGTGAAATACTGGATGAAGCA
GAGGTGATGACCCCTTTGAAATTAAAAAGCCAAGATGTTCATGGAGAAATTATAAAACAA
TATCTGGGAAATTTGATGCTTCCTAATCGGGTGTAAATGGGATTTTAAATGATGAACATT
TTGAATTTCCAATGACCATTATGTAAAGTTTTTAAACACAGTAGAGACATCATAAATTGA
AGC**ATGTTCTCACAGAAAACAAACTACAGCCATTTGTTTACTTTTTCAATTATTTTTTAT**
GTGGAAATAGTAACAGGAATCTTAGGAAATGGATTCATAGCACTAGTGAATATCATGGAC
TGGCTCAAGAGGAGGAGGATCTCTACTGCAGATCAGATTCTCACTGCTTTGGCCCTTACC
AGACTCATTTATGTGTGGTCTGTACTCATTTGTATATTGTTACTATTTCTGTGCCCACAT
TTGTCTATGAGACCAGAAATGTTTACAGCGATAGGTGTTATCTGGGTAGTGGATAACCAC
TTCAGCATCTGGCTTGCTACATGTCTTGGTGTCTTTTATTTCCTCAAAATAGCCAGTTTT
TCTAACTCTTTGTTTCTTTACCTAAAGTGGAGAGTTAAAAAAGTGGTTTTAATGATAATA
CTGATATCACTGATTTTCTTGATGTTAAACATTTCATCATTAGGGATGTATGATCATTTC
TCAATTGATGTTTATGAAGGTAATATGTCTTATAATTTGGTGGATTCAACACATTTTCCC
AGAATTTTCTTATTCACAAACTCATCTAAGGTCTTCTTAATCGCCAATTCATCCCATGTT
TTCTTACCCATCAACTCACTCTTCATGCTCATACCCTTCACAGTTTCCCTGGTAGCTTTT
TTCGTGCTCTTTCTCTCACTGTGGAAGCATCACAAGAAGATGCAGGTCAATGCCAAAGGA
CCCAGAGATGCCAGCACCATGGCCCACACAAAAGCCTTGCAAATTGGGTTCTCCTTCCTC
CTGCTGTATGCAATATACTTACTTTTCATTATCACAGGAATTTTGAACCTTGACTTGATG

AGATGTATAGTAATACTTTTATTTGACCACATATCTGGAGCAGTTTTTTCTATAAGCCAC
TCATTTGTGCTGATTCTGGGAAACAGTAAGCTGAGACAAGCCACTCTTTCTGTGCTGCCT
TGTCTTAGGTGCCGGTCCAAAGATATGGACACTGTCGTTTTCTAATAAATTCCAGAGTAC
ATTATGCAAAATCTTGAGGGTGATCAGTTCATAGAAAAAGTAATCTTAGAGGGGAAAATA
AAATATTGGGGCTTCAAATGTTGGATGGGTAATACATAGGAAGGCAGGACAAGGATGAAG
GAGACTAGCATTATATAAGTGATTTCACAGGGGAAATGGGAAAGAGGGCTTTTATATAAT
GAAGAAGAAGATAAATGATGAAGGATGAGGAAGAGTTAAATATGTAAAATGACAATAGAG
ATGGCATCATGCCGTTTTAAGAAATTTGGAATGCATATGTATGTTTATATATTTTTTAAT
TTTTATTGAATATATTTATTTACATTTTAAATGTTATCCTGTTTCCCCCACCCAACCTCC
CACCTCTTCCCACCTCCTTGCCCTGACATTCCCCTGCACTGGGGAATCCAGCCTTGACAG
GACCAAGGGCTTCTCCTCCCTTTGTTGCCAACAAGGCCATTCTTTGCTACATGTGCAGCA
GGAGCCATGGATCTGTCTATGTGTACTCTTTGGATGGTGGTTTAGTCCCTGGGAGCTCTT
GTTGGTTGGTATTGTTGTTCTTATGGTGTTGCAACTCCCTTCAGCTCCTTCAATCCTTCC
TGTAACTCCTCCAATGTGGACCCTGTTCTCAGTCCAATGGTTGACTATGAGCATTCACCT
CTGTGATTGTCATGCTCTGGCACAGCTTCTCAGAAGACAGCTACATCAGTCTCCTATAAG
AGTGCACTTCATGGCATCAGCAATGTTGTCTTGATTTGGTGTCTGTATGTATATGGGCTG
GATCCCAGGTGGGGCAGGCGCTGAATGGTCATTCCTTCAGTCTTTGCTCCAAACTTTGTC
TTTATATCTCCTATGAATATTTTTGTTCCCCCTTATAAGAATGACTGAAGTATCCACACT
TTGGCCATCCTTCTTCATGAGCTTCATGTGGTCTGTGAATTGTACATTGTGTAATCCAAG
CTTTTGGGCTAATATCCAATTATAGTGAGTGCATACCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO:81

Rat T2R03 amino acid sequence

MVPTQVTIFSIIMYVLESLVIIVQSCTTVAVLFREWMHFQRLSPVEIILISLGISHFCLQ
WTSMLYNFGTYSRPVLLFWKVSVVWEFMNVLTFWLTSLLAVLYCVKVSSFSHPVFLWLRL
KILKLVLWLLLGALIASCLSIIPSVVKYHIQMELLTLDHLPKNSSLILRLQMFEWYFSNP
FKMIGFGVPFLVFLISIILLTVSLVQHWGQMKHYSSSSSSLRAQCTVLKSLATFFIFFTS
YFLTIVVSFIGTVFDKKSWFWVCEAVIYGLVCIHFTSLMMSNPTLKKALRLQFWSPESS

SEQ ID NO:82

Rat T2R03 nucleotide sequence

GCATGGTGCCAACCCAAGTCACCATCTTCTCTATCATCATGTATGTGCTTGAGTCCTTAG
TCATAATTGTGCAAAGTTGCACAACGGTTGCAGTGCTGTTCAGAGAGTGGATGCACTTTC
AAAGACTGTCGCCGGTGGAAATAATTCTCATCAGCCTGGGCATTTCACATTTCTGTCTAC
AGTGGACATCGATGCTGTACAACTTTGGTACCTACTCTAGGCCTGTCCTTTTATTTTGGA
AGGTATCGGTCGTCTGGGAGTTCATGAACGTTTTGACATTCTGGCTAACCAGTTTGCTTG
CTGTCCTCTACTGTGTCAAGGTCTCTTCCTTCTCTCACCCCGTCTTCCTCTGGCTGAGGT
TGAAAATTTTGAAACTGGTTCTCTGGTTGCTATTGGGCGCTCTGATAGCTTCTTGTTTGT
CAATCATCCCTTCTGTTGTTAAATATCATATCCAGATGGAATTACTCACCCTAGATCATT
TACCCAAAAACAGTTCTTTGATTCTAAGACTGCAAATGTTCGAGTGGTATTTTTCTAATC
CTTTCAAAATGATTGGGTTTGGCGTTCCTTTCCTCGTGTTCCTGATTTCTATCATCTTAC
TCACAGTCTCGCTGGTCCAGCATTGGGGGCAGATGAAACACTACAGCAGCAGCAGCTCCA
GCCTGAGAGCTCAGTGCACTGTTCTGAAGTCTCTTGCCACCTTCTTCATCTTCTTCACAT
CCTATTTTCTGACTATAGTCGTCTCCTTTATTGGCACCGTGTTTGATAAGAAGTCATGGT
TCTGGGTCTGCGAAGCTGTCATCTATGGTTTAGTCTGTATTCACTTCACTTCCCTGATGA
TGAGCAACCCTACACTGAAAAAAGCACTCAGGTTGCAGTTCTGGAGCCCAGAGTCTTCCT
AAGGCAGGGAATTCAGTGAAGCCTCTGGGGTAAGGAGGCTTTGCATTGGCACAGTTCTTA
GAGTGAAATGCAAACGTGGACACGAACTTCATTCTCTTTCATGTCCACAGATGGATGGAT
CTATAAATCATCACCAATCTTCCCTGTATTCTGACCCATCCTTTTCCTGTCCTATCCATA
GTCCCCAGGTTGGTTTTGATTTTTCTCATGATCACACCTTAGCTTTAGCCACCGTTGCAA
TATCAAACATGATCTATATGTTACAGCCAAAATCATTCTCACAATTGTCAATTGCTTCAC
AAATTCAGATAAATCCCCCTTCCTGTCAGGAATGTATTGTCTGTGCATTCAATGCTCACC
ATGCTAAGCCATTCATTCCCTTCCTAACTTGAGTTTAAGAAGAAAATGTCTTACTGTTGC
CCATGTCCTATTGTGCTGCTTCTGGATGTTTTATGCAGTGATTTAGACACACGCCCTTGC
CTGTCTCCAAATACTGGCCCTTTATTCCTTTATAAGTCTAGTAGAAAATGAACTCGTCTT
TACTTCATTGACGAAGACATTGTATTCTTCCCCAAAATAGTGTTTAACTACTCTAGTCTC
ATCCATAATATCCCTAAATATCAGTGATTTCAGTGAGTAAAACCTGACAACAGTTATTGC
TTTGACTCTTAATTCAATTGTGCTGTAACATAGAGGAAACATTCTAGAACATTTCCATAT
TAATTTGTGCTTGTAGCAAACCAAAATTCTCCCCAGTTGGGTAAAAATATCAAAAGCACA
GAGTAATCAATTTTGAAATCACTCAGAAGACATCATTGTTCTATATATGTTTTTTTTAAA
CTTCCCTCTAACAAGTATCAGATCTTTGCCTTTACAGGGTCTGGTCTTACCATGACTATA
TTTTATCACCATGACCTATTTTCTCTTCATCTCTTTGTTTTCACTAACTCAGTAGCAACC
AAATATCACATTAATAGCTAACTCTGGGCACTTATTTCTCAGCCTTTATCTATTCCAGAC

ACTTTCAATGTATTTCTGCTAAACACAATGACATCTCTTTTTGTGTTCTAACGACAAGGA
ATCATAACTTTCCAACTTTTATACATGGTAGACATATTTGGTGAACTTAACTTCTGACTC
TTTCTTTAGAAGACTGAAACTACTCCGGAAAGCAAGCCTTCTGATGGAGAAATAGATACG
GGTATCGTGATTCATTGTGAAAGTGAATTCCGGTGCCTGGAAAGAAATGGATATTTTTTT
TTCTCTTGAGTGTGTCACTCTGACATATGTTCCATGTTGAATCCATATTTGATACTGATA
GCATGAATGTAAGTAAAGCATGTATGTAAGTAAAGACTGCTACCAAAACTTCGATTCAAC
TTTCCTCAGCAGTATCCCTGATATTGCATAAGAAAGAAAAAACACGCTGTCCTACTTGAA
GAAGGACGTGTTCCATGCAATGTGGATGTGTCCCAGGCTACATTGGCTCAACTGCAGCTG
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TTCTGAGCAGAGTAAATGTAAGCAATGTGGCCAAGGTCTCCTAGGAATGGGTTGTAAGCT
TGTAAGGAGTTGGGTTGTAAGAGTTTGGGATCCTTTCAGAATGGATTGAGCAAGAGCCAC
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CAAAATCTCAGATAGCTGGAAGGAAGAAGGACTGTTCTCTTTACAAGTATATAAATAGAG
AATGAGCTAAAAAGGACCCCCTCACCCCCGCCGTCACACACAGGAATACTATTCCAGAAA
CTAGGGAGTATTTTTAGTGTTCTCACTATTTCCCTTTGAAAAAAGTGCAATGGAAAACTT
ATCCATGACATACATGAGGTTGGAGTGATAAAAACAGCTGAAGGAAGAGGAAGTCTGAAA
AAAGATGGAAACAGCAATGATGCTTGTCCTATATATGTGTGACACCCACTAGTTCCCAAG
GAAACCTTACATCCATTATCTCATTTCAAGCTGGAAGGACAAGTCAAGATCACTCAACCG
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GTGGCCAAGAACAAGGAAAATCTCCAGTTAGCTTGGCACTTAGGGGCCAACATGTTTCTG
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CATCCAGTGGCCCCCATGATCCTGGTGAATGACTTGTAATACTGTGGAGACTGGCAACGA
CGGTGAATTCCTAGTAACACTTACCATAGAATCTGTTCATAATTAGACTCGCCCAGATTT
TAGTTGCTAGAGAACAATCTTTCTCCTTTACCCACATTCCTACTGAGTAGGATGCATAGG
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GTCTCCGAAACACCTGCCAAGTCCTAACTCCCAACAGTCTACAGTGTAAACCTCAGTGTT
TGCATGAGGTTTATGTATCTCCTTACCATTTCCTAAATGTCAATACCCGTGCACAGGATA
TTTGCATAGGCTGCCTCCAAGCCTGGGAAACACTCTCCTCCTCGCATTTGCTGGGTTTCA
CCTTTCCAATTCAGTGTGCCCTTTAAAAGGCACTGCTTTTCTAGGCCCACCACTATTGCT

GCTCACGCATGAACATCAAATCTACCACAGGCTTTTGCCTCTCAGAATTATTCTTCTTTC
TACTATGCAATGTGGTATCCATGAGAACTTTGTCACATTGTCAAATTCTACCTTTGTTTT
AATGnGnGCCTTTGTAATAGnGACTATGCCCAGAAATTAAATTATAGTAAGATGGGTAAC
AACnCTTCAATTnTGGAATTTATAATTAAATAAATATTATGTAATATTATGACTTATTAT
AAnGTCAATCTACTGTACCCTACTCCTACTAGGAATGCAAAGACAAATAGCAATGTGATC
AGCATGTGCTCTTTCACAAGATCATATTGTGCATGTTGCTGATGATGCCCACAGTGCATC
TATCAGAATATCTCTGATCATTTTTTTTTTTTGCTTTTGAGAAGCCCCGGTTGGTGCTG
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TCATTCCCAAGGAACAGTAAAAGCAGAAAAGGCTCTTATGTTCTAAAGAACAGAAAATAG
CCTGCATTTCAACTACCTCCTGTTCAGAAGGCACCGAAACACACCACCAAGCAAGACACC
CCTTTACTTTCTCCTGCTTCCCTCAATTTGATGATCATTTGGAAATAAGAAGAAAGAAAA
AGATGTGGAAGCCAATTAAAAACAGTCTTGTCTATCTCCCTGGTGAGCTCTCAACTTCTT
AGTCAGACCAAAGTAGGTGAAAAAATAATAATTTTTAATTTGGTATGAGAGTCATGTTTA
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TGAGGGCTCTTTTTTTGTTTTGCCTAATCATTACATTTGTTATAAGAAGTCTAAAAGTTG
GTATGCTACAGGTCTTGTCATATTTTCTCTGAGGTTGAGTGCCAAGTAGTCTGCATTGTG
TTTAAATCCTGCTTAAAATTATCCCAAGACAATATAACTTCTCAGGAGCTAAGCCAAGGG
CCCCTTTCAGACTACCTTAGTCCTCTCTCACCGTTGTCACCGTGGCTCATACATCAGAAT
CCTGAGGGAGCATCATGAAATCTAAGGCTTTACAACAGAATCTTTCTATCCCTGGTAGAA
ATCTTTTAACCTTGGGTTTTATTCTCATGCCATTCTGATGCTCGTATTTAAATTTTATGT
GTTTTTTCATATGTTCTTGCATTTCTATCGTTAAATTATGGTGACATACTTTCAAATGCT
TTGTTATTTTAAAAAGGGACAAAGAGAGATAGAAAGACAGGGAAAGATAGACAGAGGCTT
GCCTAATACAGTCAAGAAAGAAGCTATCAAAAGTATTTAGCAATACAACATTTATGATAT
ATTCATAACTGTTAACCATTTTTAATATTCTAAAATTTCACTTTTGTTTCAGAAATGTAT
ATTAAGAGAATCTGAGAAACATTTTTTTCTCATAGATGTAGAAAAACACACAAAATAAGG
TATAACACATTTAAGTGATTGAAAATAAAAACAAAAGCTTGCAAACAGGAGGAAAAGTAC
ATTGTAGGCTTTCGACATGGAGCTGCTACTAGGACCCAGGACTTGTTTATCATTTATTTG
CCAAGTCCCACAAACTCAGGGCAATACATCTCTGAGACAGTTTCCTATATTTTAATAAAA
CTTCCAAAATTGATACTCAGTGTGAATTGGCTAGCTTTAATGGCAGTCATTGGATAAACA
ATTCCAATGCCAAATTTCCCTAAGTTGATATATTTGATTAATATGTATATTAAAACATCA
GGCTATCCATCGGTTGGATCAAATACATTCTTTAGGGATCCATTCTTTTCCTTAAATTTG
ACTTATATGTGGATTCTTTTCACAATAAATAAGTAAATGAGCATTTATTTTAAAACTATT
TTAGACGGAACTGAATTACAGCCAAGGTAGTCAAAATGACTGAGAATAATCACTTACATA

TTTACAAGGGAAAGTGACTCTTCAGATTTAAGTTTAAAATTAGAAGAGAGATAAATTTCA
CAAGCTTTCACTCCTAAGGCTAAAGATAGGCTGTGTAGGTAGTTATTTCTGAGCACATTG
GCACATCACCATTGTCAGTACTTGAGGGTTTGAATGAAGCTCACTCAAAGAACTTGGAAA
GAAGGTGGTCTTCTGACATCAATCAAGAAACAAGCTTTCCTCCCTACTTCTTCCCTAAAT
GCAACAACCTAAGAATTATCCACAAGATGGATGGCGCAAGGGTTCCTCAATCAATTTCAG
GATGTACATCAATGCGCAGCCTATACTACACCGAAAAGGAAGCGCATGGGTCTTAAAAAG
TAAAGGGGATATCAAAAAATTCGCAACCAAACAAAAAGTGGCACACATTTAAGCTAGGTC
TATGTTTGGTCAGTTACACCTGGAGAAGGGGGACATTTGGTCAGCTCATTCGAACACTGT
CAAGTCCTACCAACAATTCCTCTATGCTATTACCCATTAAACCTCAGGTCTCATCGAAAA
AAAAAAAAAAAA

SEQ ID NO:83

Rat T2R04 amino acid sequence

MLSAAEGILLCVVTSEAVLGVLGDTFIALANCMEYAKNKKLSKIGFILIGLAISRIGVVW
IIILQGYMQVFFPHILTFGNITEYITYIWVFLNHLSVWFATNLNILYFLKIANFSNSVFL
WLKSRVRVVFIFLSGCLLTSWLLCFPQFSKMLNNSKMYWGNTSWLQQQKNVFLINQSLTN
LGIFFFIIVSLITCFLLIVFLWRHIRQMHSDGSGLRDLNTEAHVKAMRVLISFAVLFILH
FVGLSIQVLCFFLPQNNLLFITGLIATCLYPCGHSIILILGNKQLKQASLKALQHLTCCE
TKRNLSVT

SEQ ID NO:84

Rat T2R04 nucleotide sequence

TGGTTCCATCACATGACAATAGGCTTGAAAAACTTGCAGATAGAGAAGACATAACCCCTC
CAACAAGAAGCCAACATATGGGACATTCTCCAGCAGATAATTTATAACAGATGCAACGGG
AGCAACTTCGAGATCTGCAAAG**ATGCTGAGTGCAGCAGAAGGCATCCTCCTTTGTGTTGT**
CACTAGTGAGGCAGTGCTGGGGGTTTTAGGAGACACATTCATTGCACTTGCAAACTGCAT
GGAGTATGCCAAGAACAAGAAGCTCTCTAAGATTGGTTTCATTCTCATTGGCTTGGCGAT
TTCCAGAATTGGTGTCGTATGGATAATAATTTTACAGGGGTATATGCAAGTATTTTTTCC
ACACATACTTACCTTTGGAAACATAACTGAATATATTACTTACATATGGGTGTTTCTCAA
TCACTTAAGTGTCTGGTTTGCTACCAACCTCAATATCCTCTACTTTCTAAAGATAGCAAA

TTTTTCCAACTCTGTATTTCTCTGGCTGAAAAGTAGAGTCCGTGTGGTTTTTATCTTTCT
GTCAGGATGCTTACTTACCTCGTGGTTACTATGTTTTCCACAATTTTCAAAGATGCTTAA
CAACAGTAAAATGTACTGGGGAAACACGTCTTGGCTCCAGCAGCAGAAAAATGTCTTCCT
TATTAACCAAAGTTTAACCAATCTGGGAATCTTCTTTTTCATTATTGTATCCCTGATTAC
CTGCTTCCTGTTGATTGTTTTCCTCTGGAGACACATCAGGCAAATGCACTCAGATGGTTC
AGGACTCAGAGACCTCAACACAGAAGCTCATGTGAAAGCCATGAGAGTTCTAATATCTTT
TGCGGTACTCTTTATCCTGCATTTCGTAGGTCTTTCCATACAAGTGCTATGCTTTTTTCT
GCCACAAAACAACCTACTCTTTATAACTGGTTTGATAGCCACATGCCTCTATCCCTGTGG
TCACTCAATCATCTTAATTCTAGGAAACAAGCAGCTGAAGCAAGCCTCCTTGAAGGCACT
GCAGCACTTAACGTGCTGTGAGACAAAAAGAAATCTCTCAGTCACATAAATGGGTTTGCC
AATTAATATCTGCCATGTTATTCCACTGATTTTTACCTGTTAGTTTCTCTGTGTCTCTGT
TTAGTTTCTGTTTCCATGATCTGTCCATTGATGAGCGTGGGGTGTTGAAATCTCCGACTA
TTGTTGTGTGAGATGAAATGTGTGCTTTGAGCTTTAGTAAGATTTCTTTTGTGAATGTAG
GTGCTTTTGCATTTGGTGCATAGATATTTAAGATTGAGAGTTCAGCTTGGTGGATTTTTC
CTTTGATGAATATGAAGTGTCCTTGCTTATCTTTTTTGATGACTTTTGATTGAACGTCAA
TTTTATTGGATATTAGATTGGCAACTCAAGATTGCTTCTTGAGGTCATTTGCTTGGAAAG
TTGTTTTTCAGCCATTTACTCTGAGGTAGTGTCTGTCTTTGTCTCTGAGGTGTGTTTCCT
GCATTCAGCAAAATGCTGGGTCCTCTTTACATATCCAGTTTGTTAGTCTATGTCTTTTTA
TTGGGGAATTGAGTCCATTGATGTTGAGAGATATTAATGAATAGTGATCATTGCTTCCTG
TTATTTTCGTTGTTAGATGTGGAATTATGTTTGTTTGTCTCTCTTTTGGTTTTATTGCAA
GGAAATTATATACTTGCTTTCTGTATGGTGTAGTTTCTCTCCTTGTGTTGCAGTTTTCCT
TCTATTATCCTTTGTAGGGCTAGATTTGAAGAAAGATATTGCATAAGCTTGGTTTTGTCA
TGGGATATCTTGGTTTCTCCATCTATGTTAATTGAGAGTTTTGCAGGATATAGTAGCCTG
GGATGACATTTGTGTTCTCTTAGGGTCTGTATGACATCTGTCCAAAATCTTCTGGCTTTC
ATAGTCTCTGGTGAGAAATCGGATGTAATTCTCATAAGTCTGCCATTATATGTCACTTGA
CCTTTTTCCCTTATTGCTTTTTATGTTCTTTCTTTGTTTTGTGCATTTGGTGTTCTGATT
ATTATGTGATGTGAGGTATTTCTCTTCTGGTCAAATCTATTTGGAGTTCTGTAGGCTTCT
TGTATGTTTATGGGCATCTCTTTCTTTAGGTTATGGATGTTTTCTTCTATAATTTTGTTG
AATATATCTACTGTCCCTTTAAGTTAGGAGCCTTCACTTTCTTCTATACCTGTTATCCTT
AGGTTTAATCTTCTCACTGGATTTCCTCGATGTTTTGGACTAGGAACTTTTTGCATTTTA
CATTATCTTTGACAGGTATTTCAATGTTTTCTATGGTATCTTCTGCCACTGAGATTCTCT
CTTCTAGCTCTTGTATAATGTTGGTGATGCTTGTACCTGTGACTCCTTGTTTCTTCCTTA
GGTTTTCTATCTCCAGGGTTGTCTCCCTTTGTGCTTTTTTTATTGCTTCTATTTCCATTC
TAAATCCTGGATGGTTTTGTTCAATTCCTTCACCTCTTTGGTTGTATTTTCCTGTAATTC

TTTCAGGGATTTTTGTGTTTCCTCTTTAAGGGCTTCTACTTGTTTACTTGTGTTGTCCTG
TATTTCTTTAAGGTAGTTATTTATGTCCTTCTTGAAGTCCTCCATCATTATCAAAAAATG
TGATTTTTAAATATAAACCTTGCTTTTCTGGTGTGTTTGGATGTCAAGTATTTTCTTTGC
TGGGAGAACTGGGCTCTGATAATGCCAAGTTGTTTGATTTCTGTTGCTTAGTTTCCTGTT
CTTGCCTCTCGCCATTGGGTTTTCTCTGGTGTTTGCTTATCTTGCTGTTTCTGAGAGTGG
CTTGACACTCTTGTAGGCATCTGTGTCAGGCCTCCTGTAGAACTGTTTCCCTGTTTTCTT
TCAGCCTTTTCTGAGAACAGGTGCTCTGATCTCAGGTGTGTAGGCATTCCTGGTGACTAT
CTTTCAGCTTTAGGAGCAGGCAGGAATCAGAAGGGTCCTGTCCCTGACTGCTCCTAGATC
CTTGCACCCAGGGGGCACAGTTAGCACTAGGCAATTCCCTCTTGTGTAGGGAATGTGGGT
AGAGGATAGTCGCCTCTGATTTCTCAGGAATGTCTGCACTTCTGAAAGTCCAGCCCTCTC
CCCCACAGGATTTAGGTGCAGGGAGCTGTTTGACCACTTCAATTCAGTCCTGGGTGTAGA
CCAGAACCACAGGTAAAAAAGAATGACTTCATTAAATTAGCAGACAAATGGGTGGAACTA
GAAAATGTCATCCTGGGCTGGAGAGATGGCTCAGTGGTTCAGACCACTGGCTGCTCTTCC
AGAGGTCCTGAGTTCAATTCCCAACAACTATATGGTGGCTACCAACCATTACAATGAGAT
CAGATGCCCTCCTCTTGTGTATCTGAAGAGAGTGACAGTGTACTTACATACATAAAATAA
ATAAATAAATCTAAAAAAATGTTAAAAAA

SEQ ID NO:85

Rat T2R05 amino acid sequence

MLGAMEGVLLSVATSEALLGIVGNTFIALVNCMDCTRNKNLYNIGFILTGLAISRICLVW
ILITEAYIKIFSPQLLSPINIIELISYLWIITSQLNVWFATSLSIFYFLKIANFSHHIFL
WLKRRINIVFAFLIGCLLMSWLFSFPVVVKMVKDKKMLYINSSWQIHMKKSELIINYVFT
NGGVFLLFIIMLIVCFLLIISLWRHSKWMQSNESGFRDLNTEVHVKTIKVLLSFIILFIL
HLIGITINVICLLVPENNLLFVFGLTIAFLYPCCHSLILILANSRLKRCFVRILQQLMCS
EEGKEFRNT

SEQ ID NO:86

Rat T2R05 nucleotide sequence

AAGAGATTTCAGATACTACCACAAACATTTTTTAAATATATGTAAGTCTTTAAAGAAAGA
AGGGAAAGCCACTCCTTTATTGAGCAGCCAATAGATTGCCATCTTAAAATTCTGTGGCAG

AAGCTATTTTAAAGATCTGCGAAG**ATGCTGGGTGCAATGGAAGGTGTCCTCCTTTCAGTT**
GCAACTAGTGAGGCTTTGCTTGGCATTGTAGGGAACACATTCATTGCACTTGTGAACTGC
ATGGACTGTACCAGGAACAAGAATCTCTATAATATTGGCTTCATTCTCACTGGCTTGGCA
ATTTCCAGAATCTGCCTCGTGTGGATCTTAATCACAGAGGCATACATAAAAATATTCTCT
CCACAGTTGCTGTCTCCTATCAACATAATTGAACTCATCAGTTATCTATGGATAATTACC
AGTCAATTGAATGTTTGGTTTGCTACCAGCCTCAGTATCTTTTATTTCCTCAAGATAGCA
AATTTTTCCCACCACATATTTCTCTGGTTAAAAAGAAGAATTAATATAGTTTTTGCCTTC
CTGATAGGGTGCTTACTTATGTCATGGCTATTTTCTTTCCCAGTAGTTGTGAAGATGGTT
AAAGATAAAAAAATGCTGTATATAAACTCATCTTGGCAAATCCACATGAAGAAAAGTGAG
TTAATCATTAACTATGTTTTCACCAATGGGGGAGTATTTTTACTTTTTATAATAATGTTA
ATTGTATGTTTTCTCTTAATTATTTCCCTTTGGAGACACAGCAAGTGGATGCAATCAAAT
GAATCAGGATTCAGAGATCTCAACACAGAAGTTCATGTGAAAACAATAAAAGTTTTATTA
TCTTTTATTATCCTTTTTATATTGCATTTAATTGGTATTACCATCAATGTCATTTGTCTG
TTAGTCCCAGAAAATAACTTGTTATTCGTGTTTGGTTTGACGATTGCATTCCTCTATCCC
TGCTGCCACTCACTTATCCTAATTCTAGCAAACAGCCGGCTGAAACGATGCTTTGTAAGG
ATACTGCAACAATTAATGTGCTCTGAGGAAGGAAAAGAATTCAGAAACACATGACAGTCT
GGAAGACAAACAATCAGAAATAGTAAGTGAAAAAAAAAAAAAAAAAA

SEQ ID NO:87

Rat T2R06 amino acid sequence

EALVGILGNAFIALVNFMGWMKNRKITAIDLILSSLAMSRICLQCIILLDCIILVQYPDT
YNRGKEMRIIDFFWTLTNHLSVWFATCLSIFYFFKIANFFHPLFLWIKWRIDKLILRTLL
ACLILSLCFSLPVTENLADDFRRCVKTKERINSTLRCKLNKAGYASVKVNLNLVMLFPFS
VSLVSFLLLILSLWRHTRQMQLNVTGYNDPSTTAHVKATKAVISFLVLFIVYCLAFLIAT
SSYFMPESELAVIWGELIALIYPSSHSFILILGNSKLKQASVRVLCRVKTMLKGRKY

SEQ ID NO:88

Rat T2R06 nucleotide sequence

GTGAGGCCTTAGTAGGAATCTTAGGAAATGCATTCATTGCATTGGTAAACTTCATGGGCT
GGATGAAGAATAGGAAGATCACTGCTATTGATTTAATCCTCTCAAGTCTGGCTATGTCCA

GGATTTGTCTACAGTGTATAATTCTATTAGATTGTATTATATTGGTGCAGTATCCAGACA
CTTACAACAGGGGTAAAGAAATGAGGATCATTGATTTCTTCTGGACGCTTACCAACCATT
TAAGTGTCTGGTTTGCCACCTGCCTCAGCATTTTCTATTTCTTCAAGATAGCAAACTTCT
TCCATCCTCTTTTCCTCTGGATAAAGTGGAGAATTGACAAGCTAATTCTGAGGACTCTAC
TGGCATGCTTGATTCTCTCCCTATGCTTTAGCCTCCCAGTCACTGAGAATTTGGCTGATG
ATTTCAGACGCTGTGTCAAGACAAAAGAAAGAATAAACTCTACTCTGAGGTGCAAATTAA
ATAAAGCTGGATATGCTTCTGTCAAGGTAAATCTCAACTTGGTCATGCTGTTCCCCTTTT
CTGTGTCCCTTGTCTCATTCCTTCTCTTGATTCTCTCCCTATGGAGACACACCAGGCAGA
TGCAACTCAATGTAACAGGGTACAATGATCCCAGCACAACAGCTCATGTGAAAGCCACAA
AAGCAGTAATTTCCTTCCTAGTTCTGTTTATTGTCTACTGCCTGGCCTTTCTTATAGCCA
CTTCCAGCTACTTTATGCCAGAGAGTGAATTAGCTGTAATTTGGGGTGAGCTGATAGCTC
TAATATATCCCTCAAGCCATTCATTTATCCTGATCCTTGGGAACAGTAAACTAAAACAGG
CATCTGTAAGGGTGCTTTGTAGAGTAAAGACTATGTTAAAGGGAAGAAAATATTAGCATC
ATGGATATATTTGAAGAAAAACTATCACTGTCTAAAGAAAAAGGATGACAAATCATTATC
TTTCATTCTTATATGAATATTGCTTTCATGCGGTAACATCTTTTAACAAACTTAAATCAA
ATGTTGGGAAATCTCATATACAGCAACTTTGCATGTCTCTCTGTCTATTTCCCTCTCCCT
TTGTACATAGTTGACATAAAAAAAGAATTTTCATGACAAAATTGTAATAAATAGCTACAG
AGGCAGCACATTTTCATAGTAAGTTCTGAATCACTCTTCCAAATGCAAAGCTGCCTGACA
AATTCAAAACAACTGTAACAGTATTTCACTGCTGTTTGCATTCTTTGGAAAAGCAGGTGG
TTTGTTCCTATGACCTGACTTGGAGTTTTCTTCTTACATCACTG

SEQ ID NO:89

Rat T2R07 amino acid sequence

MGSSLYDILTIVMIAEFIFGNVTNGFIVLTNCIAWLSKRTLSFIGWIQLFLAISRVVLIW
EMLLAWLKYMKYSFSYLAGTELRVMMLTWVVSNHFSLWLATILSIFYLLKIASFSRPVFL
YLKWRVKKVLLLILLGNLIFLMFNILQINTHIEDWMDQYKRNITWDSRVNEFVGFSNLVL
LEMIMFSVTPFTVALVSFILLIFSLWKHLQKMHLSSRGERDPSTKAHVNALRIMVSFLLL
YATYFISFFISLIPMAHKKGLDLMFSLTVGLFYPSSHSFILILGHSNLRHSSCLVITYLR
CKEKD

SEQ ID NO:90

Rat T2R07 nucleotide sequence

CAGTAGCAAAATTTTACTATGTTCATTGATATTATGTCAnGnCACTACGTAAGAAGGAAG
ACTTGAAAGAAAGCTTATCTGAGTTTTTAAGAATACATGGACATTTCAGCTTGGCAAATG
ACGAGCTGTGAATTTTTGTCATCTGGAC**ATGGGAAGCAGCCTGTATGATATCTTAACTAT**
TGTCATGATTGCAGAGTTTATATTCGGAAATGTGACCAATGGATTCATAGTGCTGACAAA
CTGTATTGCTTGGCTCAGTAAAAGAACTCTTTCTTTCATTGGTTGGATCCAGCTTTTCTT
GGCCATTTCCAGAGTGGTTTTGATATGGGAAATGTTACTAGCATGGCTGAAATATATGAA
GTATTCATTTTCATATTTGGCTGGCACAGAATTAAGGGTTATGATGTTGACCTGGGTAGT
TTCCAATCACTTTAGTCTCTGGCTTGCCACCATTCTAAGCATCTTTTATTTGCTCAAAAT
AGCTAGTTTCTCCAGACCTGTTTTCCTGTATCTGAAGTGGAGAGTAAAAAAAGTGCTCCT
GCTGATTCTTCTCGGAAATTTAATCTTCCTGATGTTCAATATATTACAAATCAACACTCA
CATAGAAGACTGGATGGATCAATATAAGAGAAATATAACGTGGGATTCCAGAGTGAATGA
ATTTGTGGGGTTTTCAAATCTGGTTTTATTGGAGATGATTATGTTCTCTGTAACACCATT
CACCGTGGCTCTGGTCTCCTTCATCCTGTTAATCTTCTCTTTATGGAAACATCTCCAGAA
GATGCATCTCAGTTCCAGAGGGGAACGAGACCCTAGCACAAAAGCCCATGTGAATGCCCT
GAGAATTATGGTCTCCTTCCTCTTACTCTATGCCACTTACTTCATATCCTTTTTTATATC
ATTAATTCCTATGGCACATAAAAAAGGACTAGATCTTATGTTTAGCCTAACTGTTGGACT
TTTCTACCCTTCAAGCCACTCATTTATCTTGATTTTGGGACATTCTAATCTAAGGCATTC
CAGTTGTCTGGTGATAACCTATCTGAGATGTAAGGAAAAGGATTAGAAATTCACTATTCC
ATAAGGCAGTTAAACCACATGCTATTAGGTATACTCAGTGCTAGATCCCTAGGCAAGCAT
TAACATTAAAAATATATAATTTCTAGATTCTTCTATTTGTGATAAACCACTCACTTAGAA
TAATGCTAAAGTAGCGTGATGTTGTATATAAGTGTAAGAATAAAATGTAATTAATTTAGT
TTAGGCACAATAACATATGTCTACTAAGTAAAAACTAGGCAGGCTGCTACACGCATATTA
GAATCCAGGCTGAGGTATATAGACTCAAGAAATACTGTGGAATAAAGATTTTAATTTTCA
TTCTATTGTGAGTTATGTGAAATCAATGCCATTAAAGGCATACACAAGATTTTCACACAC
TGAAACAACTTCTTGCATTTTGTCATATTGTATTGGAAGTAAATTGGAGATAAACTTAAT
ATCAATAAATTACAAAATGTAAACATAAACAGGGTGATTAAAAATTAGCCTCTAGGTCCT
GGGGAAATGATTCaAGTAAAGTGCTTTCTTTTCAAATAGGAGAATCTGATTGTAAATCAT
CTAAAAGTCTGGCATAAAATGTCAATGAAAATTGTATGTAAAATATAGCTATgGCmAAGA
GCACCmAAGAAAAGAAAATTTTTGCCTTTGAAACCCAGTAATTGATATCCTTTAAAAAAG
CAGTTACATATTTTTCTGTTTAAGATTTTGTCAAAGGGTAGCTTTGACAACTAATATAAG
CTGAGGAAGGTAGCAAGTGTGAAGTCAGCTAATGGGGTCAGTCAAGTGCTGTTAGCAGCA
GATGGAGGCCACTGCTGAATTTAGCAGGCAATTTACAGGGTGAGCACTGCTAGTGCTGAC

AGAAGAAAAACTCTGAAATTTTAACTCTTTAGGGTCTGGTGAGAAAGAAAAAGAGAGAAA
ATCGCATATATATATATATATATATATATATATATATATATATATATATATATATATATA
TCATGGAAGCTCTAACAAGTTGACTCAAACAACTTTATGATGTTTTTAGGCCCTTTTATT
TTAATGTCAGTGAATTAGGTGTGGTACAGCAATATTGCTACTTTTAAATTCAAAGCAGTT
GTTTTATATATTATTCATTATATAAGCTAATTATAAGTTTAAATCAAAAGGTTTATTTGT
CCATGATTTTACTTTATCATTGGGCACACCTGTGCTCTCATCCTTGGGCTTGACCTAGAA
TGAAAGTTTATCCTTGATCATATGTCTGTCACAAGACTACTTCTCTTCCTATAGTAGTTT
ATGTACTTACAATATACAAAAGTTTATTGAATTCCTTTTATCACTTATGCAGCCTTTTCT
TACTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTA
TTCTATTCTATTCTATTCTAGAATCTAACCTATACATTCATTTCTGGCAAAACAACTTAT
ATCATCTCCTTAATTATTTTATCAATTAATCTAACATCCTGAAGTTATTTAAATCTAATA
TAAGGACTCTGTAAAGTCACAAATTTATTTATACTTCACAAAATTCATTATTTTATGGAA
CTGCAGCATTGCCTGGGCCAGGAGTCACAAGAGTTCCAGAGTTGACTTTATTGGCATCTG
CCTGGCTAACTGAAGGATCAGTTTTCTGTGTACAATAATTTTGTGTATCTCTTTTGATGC
AAGATATGAAAAATAATTTCAGTCTAAAAGTGTCCTTAAATTTGAAACTCTCTGGCCAGA
ATCTAACTATTGATGACCAGTTTGCACCATGGACTCAGTGTCTTCTATTGCTTTAAAATA
AGCAACATCTTGAATGCTTTTCTTGTGTATTAGGCAAATAATTAACAACATGTTTCTATG
ATTGTCTCAATAACAATACTATATTTCTCACAGTTTTTAATTTTTATGGCAAAGTTGGCT
AATAAGAATTTTTTTCAAATTATCAAACGTGAAGAAAACTTGACATTTTATTTCATGGAG
ATTCTAAATGTTTTCTTAGCATATTGCCTTTTTACTAACTTGATTTTTATCATGTTTTGG
TAGTATTTCTAATTTTCCTTTTTTTCTAAGTATGTTATGTAGTAACACCAGGAGAATGAA
ACAAATGACATTTATACTAAGGATGTGACAAATAAGGCCCAAAGAAAGTTTTGAAAATCA
TGATCTCATTTCTATTCTTCTTTATTAAGTATAGCATAAGCAAAATTCTGATGGTGGTCT
TGGCCCATATCTTTGAACACAGTGTAGTGGTGAAGACTTTTTCAAATATTATGTCATATT
TGTACCCATCTCTGTACCTATTTCTTCTGATTTCATGAGGAAAAAATGAGGAAGGGTTTG
TTTGTGTGCTGGAGCAGCTGAAGTGGACCAAGGGGCAGGAATTCTCTCTGTTCGGTCCTA
GTGTGACTGATGATGCTCTCATTGAAAAACAGGAAGAAGAAGAAAGACTTTATATGCACC
ATTCACTCCTTCCCCCTCCTACATTCCACCTCCCTCTTGAAAGAGTGTCTATCTATATAG
ATATAGCTATCCTGAAATCCATTAAGTAGACCTGACTGGCTTAAATCTCACAGAAATTCA
CCTACCTTTTCCATGATTGCTGAAATTAAAGACATGTGCCGACATATTGGGCACATTCAG
ACCTTTTGCCAACTGTCTTTCAACTCATTTGGACCTACTGAGAAGTATTCAAAATATTTG
GTTGTTTTAAATAAAAGGAAAGTGGGTCTATATTACTTGAATTGGATAGAGAAATTTTCA
CTTACAAGTGATATTGAAAATGGGGGAGAATGTATTTTAGCATAAGCACCAGAACACAAA

GCAATTCTTGTTAAAACTTTATCGATAAATTGGATAAATGTTAAAAAAGAAAAAATAAAA
TATACGAACTATTATGAAAAAAAAAAAAAAAAAA

SEQ ID NO:91

Rat T2R08 amino acid sequence

MEPVIHVFATLLIHVEFIFGNLSNGLIVLSNFWDWVVKRKLSTIDKILLTLAISRITLIW
EMYACFKIVYGSSSFIFGMKLQILYFAWILSSHFSLWFATALSIFYLLRIANCSWKIFLY
LKWRLKQVIVGMLLASLVFLPGILMQRTLEERPYQYGGNTSEDSMETDFAKFTELILFNM
TIFSVIPFSLALISFLLLIFSLWKHLQKMQLSSRGHGDPSTKAHRNALRIMVSFLLLYTS
YFLSLLISWIAQKHHSKLVDIIGIITELMYPSVHSFILILGNSKLKQTSLWILSHLKCRL
KGENILTPSGKPIN

SEQ ID NO:92

Rat T2R08 nucleotide sequence

CTGCAGGTTGGTGATCCAGTAATGAGCAGCACTGTTATATCTCAGGCTTTCTAAGATCAT
GGAACCTGTCATTCACGTCTTTGCCACTCTACTAATACATGTGGAGTTCATTTTTGGGAA
TCTGAGCAATGGATTAATAGTGTTGTCAAACTTCTGGGACTGGGTCGTTAAACGAAAACT
TTCCACAATTGATAAAATTCTTCTTACATTGGCAATTTCAAGAATCACTCTCATCTGGGA
AATGTATGCTTGTTTTAAAATTGTATATGGTTCATCTTCATTTATATTTGGGATGAAGTT
ACAAATTCTTTATTTTGCCTGGATCCTTTCTAGTCACTTCAGCCTCTGGTTTGCCACAGC
TCTCAGCATCTTTTACTTACTCAGAATAGCTAACTGCTCCTGGAAGATCTTCCTGTATCT
GAAATGGAGACTTAAACAAGTGATTGTGGGGATGTTGCTGGCAAGCTTGGTGTTCTTGCC
TGGAATCCTGATGCAAAGGACTCTTGAAGAGAGGCCCTATCAATATGGAGGAAACACAAG
TGAGGATTCCATGGAAACTGACTTTGCAAAGTTTACAGAGCTGATTCTTTTCAACATGAC
TATATTCTCTGTAATACCATTTTCATTGGCCTTGATTTCTTTTCTCCTGCTAATCTTCTC
TTTGTGGAAACATCTCCAGAAGATGCAGCTCAGTTCCAGAGGACATGGAGACCCTAGCAC
CAAGGCCCACAGAAATGCTTTGAGAATTATGGTCTCCTTCCTCTTGCTCTACACTTCATA
TTTCCTGTCTCTTCTTATATCATGGATTGCTCAGAAGCATCACAGTAAACTGGTTGACAT
TATTGGTATTATTACTGAACTCATGTATCCTTCAGTCCACTCATTTATCCTGATTCTAGG
AAATTCTAAATTAAAGCAGACTTCTCTTTGGATACTGAGTCATTTGAAATGTAGACTGAA

AGGAGAGAATATTTTAACTCCATCTGGCAAACCAATTAACTAGCTGTTATATATTCTGTA
TTGCAAACAAATCAGTGAGTTAGTGGTTCAAGGATTCCATCCTTGACTTATTGTATCATG
GAAGTCATATAGGGAGAGGCTGAACAAGCTATCTTCTGTAAATTGGCAAGGGTTGCATAT
AGTACTGGTACTGGGACACCATCCAACCATAAAACCTTCTAACCATAACCTACCTGACTG
CAAGATATGCTGGGACAATGGTGGCTCAGAGATTTTGGGACTGGCCAACCAATGTCTATT
CTTTCTTGAGGCTCACTCAATAAGGAGGCCATGCCCAACTCGTCcTGGATGGCCAGGAAC
CAGAATCTCTGATGGsCCAATGATCTATGGnAGAACCCAGCATTACTGGGAAAAAAGAAT
AATCACTTTGATGAATGGTCAAATATTTCCTAAATATATTCTGATACACTTGTACATCAT
TTCTCTTTCCCAATCATCATCACAGGGACTTCTCCCCAGCACCTGATGGGAACAGATACC
AAAATCTACAGCCAAATACTAAATGCAGGTTGGGGAACTCCACAAAAGACTGGAAGGAAG
TACTGTGAGAGCCAGAGTGGTCCAGAACACTAGGAGAACACAGAACATCGAATTAACTAA
GCAGCACTCATAGGGTTAATGTAAAATAAAGCAGCAGTCACATAGACTGCACAGGTGTAC
TCTAGATCCTCTGCATATATGTTGTGGTTGTCAAACTTGGGAGTTTTGTTGGACTAATAA
CAATGTGAATAAGTAAGTCTCTGACACTTATTCCCGCTCTTGGAACCCTTTTCCACATTT
TGTATTGTCTTACCACCTTGATATGAAGGTTTCTGAATAGTCCAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO:93

Rat T2R09 amino acid sequence

MLSAAEGILLSIATVEAGLGVLGNTFIALVNCMDWAKNKKLSKIGFLLFGLATSRIFIVW
ILILDAYAKLFFPGKYLSKSLTEIISCIWMTVNHMTVWFATSLSIFYFLKIANFSHYIFL
WLKRRTDKVFAFLLWCLLISWAISFSFTVKVMKSNPKNHGNRTSGTHWEKREFTSNYVLI
NIGVISLLIMTLTACFLLIISLWKHSRQMQSNVSGFRDLNTEAHVKAIKFLISFIILFIL
YFIGVAVEIICMFIPENKLLFIFGLTTASVYPCCHSVILILTNSQLKQAFVKVLEGLKFS
ENGKDLRAT

SEQ ID NO:94

Rat T2R09 nucleotide sequence

GGACACTGCAGCAGATCTGCTATAGAATAACAGATACAAACATAGCAACCTGCAGAG**ATG**
CTCAGTGCAGCAGAAGGCATCCTTCTTTCCATTGCAACTGTTGAAGCTGGGCTGGGAGTT

TTAGGGAACACATTTATCGCCCTGGTTAACTGCATGGATTGGGCCAAGAACAAGAAGCTC
TCTAAGATTGGTTTCCTTCTCTTTGGCTTAGCAACTTCCAGAATTTTTATTGTATGGATA
TTAATTTTAGACGCATATGCAAAGCTATTCTTTCCGGGGAAGTATTTGTCTAAGAGTCTG
ACTGAAATCATCTCTTGTATATGGATGACTGTGAATCACATGACTGTCTGGTTTGCCACC
AGCCTCAGCATCTTCTATTTCCTAAAAATAGCAAATTTTTCCCACTATATATTTCTCTGG
TTAAAGAGGAGAACTGATAAAGTATTTGCCTTTCTCTTGTGGTGTTTATTAATTTCATGG
GCAATCTCCTTCTCATTCACTGTGAAAGTGATGAAGAGCAATCCAAAGAATCATGGAAAC
AGGACCAGTGGGACACATTGGGAGAAGAGAGAATTCACAAGTAACTATGTTTTAATCAAT
ATTGGAGTCATTTCTCTCTTGATCATGACCTTAACTGCATGTTTCTTGTTAATTATTTCA
CTTTGGAAACACAGCAGGCAGATGCAGTCTAATGTTTCAGGATTCAGAGATCTCAACACT
GAAGCTCATGTGAAAGCCATAAAATTTTTAATTTCATTTATCATCCTTTTCATCTTGTAC
TTTATAGGTGTTGCAGTAGAAATCATCTGCATGTTTATCCCAGAAAACAAACTGCTATTT
ATTTTTGGTTTGACAACTGCATCCGTCTATCCCTGCTGTCACTCAGTCATTCTAATTCTA
ACAAACAGCCAGCTGAAGCAAGCCTTTGTAAAGGTACTGGAGGGATTAAAGTTCTCTGAG
AACGGAAAAGATCTCAGGGCCACATGAGTCTGGAACAGAAATGGGTAGTCTGGAATAATT
GTAAGGAAGTCGTAGAAGGTCTTTTTCATTTGTACAGTGCTCTTACCTTGTTTTTGAGGA
GATGTAAACTTTTTTATTTTTATTTTTTATCCTATGTGAATAAGTGTGTGTGTGTGTGTG
TGTGTTTATGTGTGTGTGTATATATGTCTATGTGTGTTTTAGGAGGTTTAAGAGGGAAGA
GGGAATAGAGGTATGTTGGTGTTTTTAACATGGATATTCACAGGCCAAGGAACTTGTTCT
CTCCTTTTACCTTAGGGTAGTGTCCTTTGTGGCTGTCACTCTGACAGTCTACACTAGTTG
AACTAAGAGCTTTTAGCCAGTTCACTTGTCTAAACCTCCCTTCTCATGGTAGCAGTGTTC
TGATTACAGAATCATGCTGTCACATACAGCTTTTTAACAAGGTTCCCATAGACAGAATTC
ATGTCAAACGGAATGCACAGCTGTCACTCTTACCCACCGATCTCTCTTGCCAGCCCATTC
CTATTGACTTTAAACTGTAGTATTAAACTTTACTGAAATCTTCTGCAACCAGTCTGACTA
TGTCTCTTGAAATCACATGATATGGTGGAATTTTAATGCCATGTGAAAATTTGTTTGTTC
AGTTAGTTTCCTACTCTGCCAAATCATTCTCTTACACTTGGCAGAAAAAAACCATCAACT
GTAGACTATTTTGTGTAAAGACTAATACAGATAGAATAAGTATCTTAATCAAGATGTCAT
TGTGATTATCCTAATTTCCCCAGAGCACTGGTTCCCTTTCCCCAGAAAGACTCACAAAGG
AACTGAGGCAAACAGTTGTGGTCACTCTTGATATTTACCAGTTGAAACTGAAGAACAGTG
TTTCCTTTCTGTTCAGTTTTACTACTTACAGTTACTTTATTTCATCCATTAAATCCCAAA
GTGCTTATTAATAGTAGATATTTGATGAAGCAACAATGGTTATAAGAGTGGATGTGGATC
TATGACAAAGATCTAGAGAAACAGACTATTTGTGAAAGATGGATGAAAGCCCTGATGAAA
GGATTCTTCATGGTCTTTGACCCCAGGGAGTTTTGAAATCAAGCAGCCACAGATCAAAGA
GAGCTGAGAAGAGGTTCTCCTGAAGAAAATATCCAAACACATGGTGCCAGCCAAAGCAGA

AAATAGTGGACAATTCAGTCCAGGACCTGAATGAGGTAGACAATGTCCTGTTAAGGGTTG
GAACAAATATATAGATATGGTCATTCATATACAGAAACCTACAGGCGTGTTTGAACTCTT
GGTTTCTCAGTAATCAATTCTTAAATCTTTTTTAGAATGGATTTTTTATCATCATTCATG
ATCTCTCAGCAGAGTCTGCAGGGGCTAAGAGACACACTAAGAGTATCTGGAGGGGGGAGT
GTCTTCCTGCTCTATCAACCCCTAAAGTCATATATAACAATACAAAATTCCACATTAGTT
AAGTTCTTTTTTTTACATCTTTATTAAATTGGGTATTTCTTATTTACATTTCAAATGTGA
TTCCCTTTCCTGGTTTCCAGGCCAATATCCCCCTAACCTCTCCCCTTCTATGTGGGTATT
CCCTCGTGCCGAATTC

SEQ ID NO:95

Rat T2R10 amino acid sequence

MFLHTIKQRDIFTLIIIFFVEITMGILGNGFIALVNIVDWIKRRRISSVDKILTTLALTR
LIYAWSMLIFILLFILGPHLIMRSEILTSMGVIWVVNNHFSIWLATCLGVFYFLKIANFS
NSLFLYLKWRVKKVVLM

SEQ ID NO:96

Rat T2R10 nucleotide sequence

CCCGGGCTGCAGGATTCGGCACGAGAATGAAAACTTTTGCTCTACTATTTTGCTGTTCTG
TGATACCACAGACCATAAAACAATCGAGCCAAGGGATCAAGAGCTGAAACTTCAGAAAGT
GGGAATCAAATTTCCTTCCTGATAGGTTAGCTTATGAGAATTCAGCATCTTATTCAACTT
CAGAAAATTGGATATAAGATACAGTGTCTGGATGAAGCCGAATTGATCTATTTGGGGAGA
AAAAACGCCAACATTTATAATAAGGTTTTATGAGACAGTTCCTGGGAAATTTGGATATTT
CCTAGTTAGTAATGTGTAAATGGGATTTTAAAACATGATTATTTTGTATTTTTAACAACC
AACATGAGGAGCTTTTTAAATGCCACTTAGACATTATAAACTGAAGC**ATGTTCTTACACA**
CAATAAAGCAACGTGATATTTTTACTTTGATAATCATATTTTTTGTGGAAATAACAATGG
GAATCTTAGGAAATGGATTCATAGCACTAGTGAACATTGTGGACTGGATCAAGAGAAGAA
GGATTTCTTCAGTGGATAAGATTCTCACTACCTTGGCCCTTACCAGACTCATTTATGCGT
GGTCTATGCTCATTTTTATATTGTTATTCATACTGGGCCCGCATTTGATTATGAGATCAG
AAATACTTACATCAATGGGTGTTATCTGGGTGGTGAACAATCACTTCAGCATCTGGCTTG

CTACATGCCTCGGTGTCTTTTATTTTCTCAAGATAGCCAATTTTTCTAACTCTTTGTTTC
TTTACCTAAAGTGGAGAGTTAAAAAAGTGGTTTTAATG

SEQ ID NO:97

Rat T2R11 amino acid sequence

GSGNGFIVSVNGSHWFKSKKISLSDFIITSLALFRIFLLWIIFTDSLIIVFSYHAHDSGI
RMQLIDVFWTFTTHFSIWLISCLSVFYCLKIATFSHPSFL*LKSR

SEQ ID NO:98

Rat T2R11 nucleotide sequence

GGATCCGGAAACGGTTTTATCGTGTCAGTCAATGGCAGCCATTGGTTCAAGAGCAAGAAG
ATTTCTTTGTCTGACTTCATCATTACCAGCTTGGCCCTCTTCAGGATCTTTCTGCTGTGG
ATCATCTTTACTGATAGCCTCATAATAGTGTTCTCTTACCACGCCCACGACTCAGGGATA
AGGATGCAACTTATTGATGTTTTCTGGACATTTACAACCCACTTCAGTATTTGGCTTATC
TCCTGTCTCAGTGTTTTCTACTGCCTGAAAATAGCCACTTTCTCCCACCCCTCATTCCTG
TAGCTCAAATCTAGA

SEQ ID NO:99

Rat T2R12 amino acid sequence

MLSTVSVFFMSIFVLLCFLGILANGFIVLMLSREWLWRGRLLPSDMILLSLGTSRFCQQC
VGLVNSFYYSLHLVEYSRSLARQLISLHMDFLNSATFWFGTWLSVLFCIKIANFSHPAFL
WLKWRFPALVPWLLLGSILVSFIVTLMFFWGNHTVYQAFLRRKFSGNTTFKEWNRRLEID
YFMPLKLVTTSIPCSLFLVSILLLINSLRRHSQRMQHNAHSLQDPNTQAHSRALKSLISF
LVLYALSYVSMVIDATVVISSDNVWYWPWQIILYLCMSVHPFILITNNLKFRGTFRQLLL
LARGFWVT

SEQ ID NO:100

Rat T2R12 nucleotide sequence

GTGTGAGGGACTGTGGGTAGGGGCTGGGAGGAGGCCAGGAACCAAGGCAACCAGTGGTGA
CAGGAGGGGCTGAA**ATGCTATCAACTGTATCAGTTTTCTTCATGTCGATCTTTGTTCTGC**
TCTGTTTCCTGGGAATCCTGGCAAACGGCTTCATTGTGCTGATGCTGAGCAGGGAATGGC
TATGGCGCGGTAGGCTGCTCCCCTCAGACATGATCCTCCTCAGTTTGGGCACCTCCCGAT
TCTGCCAGCAGTGCGTTGGGCTGGTGAACAGTTTCTACTATTCCCTCCACCTTGTTGAGT
ACTCCAGGAGCCTTGCCCGTCAACTCATTAGTCTTCACATGGACTTCTTGAACTCAGCCA
CTTTCTGGTTTGGCACCTGGCTCAGCGTCCTGTTCTGTATCAAGATTGCTAACTTCTCCC
ATCCTGCCTTCCTGTGGTTGAAGTGGAGATTCCCAGCATTGGTGCCTTGGCTCCTACTGG
GCTCTATCTTGGTGTCCTTCATCGTAACTCTGATGTTCTTTTGGGGAAACCACACTGTCT
ATCAGGCATTCTTAAGGAGAAAGTTTTCTGGGAACACAACCTTTAAGGAGTGGAACAGAA
GGCTGGAAATAGACTATTTCATGCCTCTGAAACTTGTCACCACGTCAATTCCTTGCTCTC
TTTTTCTAGTCTCAATTTTGCTGTTGATCAATTCTCTCAGAAGGCATTCACAAAGAATGC
AGCACAATGCTCACAGCTTGCAAGACCCCAACACCCAGGCTCACAGCAGAGCCCTGAAGT
CACTCATCTCATTTCTGGTTCTTTACGCGCTGTCCTATGTGTCCATGGTCATTGACGCTA
CAGTTGTCATCTCCTCAGATAACGTGTGGTATTGGCCCTGGCAAATTATACTTTACTTGT
GCATGTCCGTACATCCATTTATCCTTATCACTAATAATCTCAAGTTCCGAGGCACCTTCA
GGCAGCTACTCCTGTTGGCCAGGGGATTCTGGGTGACCTAGAAGGTTTGGTCTCTTTATC
TGTACCCTTTGAAGAGACTTAGGTGAGGGTGACTTCCCTTGGAAGTGATCTCATCTACAT
GGAAATGTCTTTGTAGGCTGACATGGGGTCATACTATGTGGTTCCTCCTTGGGAAAGAGG
AGAAGAAAATACAGGGATTCTGAGCGTTCTTCCTTATCTTGGGATATTATGAAAATGGAC
ATTCTGAATCCTGAACCAGTATTGATCTGAAGTGCAAAGTACAATATGCCTGTTCCCTTC
ATGTCTGCTATCCTCTTGGTACTTATTAATTCCCT

SEQ ID NO:101

Rat T2R13 amino acid sequence

MCGFPLSIQLLTGLVQMYVILIIAVFTPGMLGNVFIGLVNYSDWVKNKKITFINFILICL
AASRISSVLVVFIDAIILELTPHVYHSYSRVKCSDIFWVITDQLSTWLATCLSIFYLLKI
AHFSHPLFLWLKWRLRGVLVGFLLFSLFSLIVYFLLLELLSIWGDIYVIPKSNLTLYSET
IKTLAFQKIIVFDMLYLVPFLVSLASLLLLFLSLVKHSQNLDRISTTSEDSRAKIHKKAM

KMLLSFLVLFIIHIFCMQLSRWLFFLFPNNRSTNFLLLTLNIFPLSHTFIIILGNSKLRQ
RAMRVLQHLKSQLQELILSLHRLSRVFTMEIA

SEQ ID NO:102

Rat T2R13 nucleotide sequence

GGGATTCAGTTGGATAAGAGAAAAGTCAAAACCCTAAGACTAAGAATTTCCTTAAGTAGA
TATCAATTTCTATCCATTGGAAGGAGTTTCCAATCACACTGAAATTACAATAAAAAAGGA
GCAAGATAACTATGGGAAAGGATGATTTTCGGTGGATGTTTGAGAACTGAGCAGCAAGGC
AAATTGATAG**ATGTGTGGATTCCCTCTTTCTATTCAACTGCTTACTGGATTGGTTCAAAT**
GTACGTGATATTGATAATAGCAGTGTTTACACCTGGAATGCTGGGGAATGTGTTCATTGG
ACTGGTAAACTACTCTGACTGGGTAAAAAACAAGAAAATCACCTTCATCAACTTCATCCT
GATCTGTTTGGCAGCGTCCAGAATCAGCTCTGTGTTGGTGGTATTTATTGATGCAATCAT
CCTAGAACTAACTCCTCATGTCTATCATTCTTACAGTCGAGTGAAATGCTCTGATATATT
CTGGGTTATAACTGACCAGCTGTCAACGTGGCTTGCCACCTGCCTCAGCATTTTCTACTT
ACTCAAAATAGCCCACTTCTCCCATCCCCTTTTCCTTTGGTTGAAGTGGAGATTGAGAGG
AGTGCTTGTTGGTTTTCTTCTATTTTCTTTGTTCTCATTGATTGTTTATTTTCTACTCCT
GGAATTACTGTCTATTTGGGGAGATATTTATGTGATCCCTAAAAGCAATCTGACTTTATA
TTCAGAAACAATTAAGACCCTTGCTTTTCAAAAGATAATTGTTTTTGATATGCTATATTT
AGTCCCATTTCTTGTGTCCCTAGCCTCATTGCTCCTTTTATTTTTATCCTTGGTGAAGCA
CTCCCAAAACCTTGACAGGATTTCTACCACCTCTGAAGATTCCAGAGCCAAGATCCACAA
GAAGGCCATGAAAATGCTATTATCTTTCCTCGTTCTCTTTATAATTCACATTTTTTGCAT
GCAGTTGTCACGGTGGTTATTCTTTTTGTTTCCAAACAACAGGTCAACTAATTTTCTTTT
GTTAACATTAAACATCTTCCCATTATCTCATACATTCATTATCATCCTGGGAAACAGCAA
GCTTCGACAAAGAGCAATGAGGGTCCTGCAACATCTTAAAAGCCAACTTCAAGAGTTGAT
CCTCTCCCTTCATAGATTGTCCAGAGTCTTCACTATGGAAATAGCTTAAAGGGGAGACTT
GGAAGGTCACTGGTAACTTGTTCTTCCGCTGAGTTCTGTTAAGTAATGCTGGACATATAT
GAACTATCCCTAGTGCATACTGATATT

SEQ ID NO:103

Rat T2R14 amino acid sequence

VANIMDWVKRRKLSAVDQLLTVLAISRITLLWSLYILKSTFSMVPNFEVAIPSTRLTNLV
WIISNHFN

SEQ ID NO:104

Rat T2R14 nucleotide sequence

CTGTGGCAAACATAATGGATTGGGTCAAGAGAAGGAAGCTCTCTGCAGTGGATCAGCTCC
TCACTGTGCTGGCCATCTCCAGAATCACTCTGTTGTGGTCATTGTACATACTGAAATCAA
CATTTTCAATGGTGCCAAACTTTGAGGTAGCTATACCGTCAACAAGACTAACTAATCTTG
TCTGGATAATTTCTAACCATTTTAAT

SEQ ID NO:105

Mouse T2R01 amino acid sequence

MQHLLKTIFVICHSTLAIILIFELIIGILGNGFMALVHCMDWVKRKKMSLVNKILTALAI
SRIFHLSLLLISLVIFFSYSDIPMTSRMTQVSNNVWIIVNHFSIWLSTCLSVLYFLKISN
FSNSFFLYLKWRVEKVVSVTLLVSLLLLILNILLINLEISICIKECQRNISCSFSSHYYA
KCHRQVIRLHIIFLSVPVVLSLSTFLLLIFSLWTLHQRMQQHVQGGRDARTTAHFKALQT
VIAFFLLYSIFILSVLIQNELLKKNLFVVFCEVVYIAFPTFHSYILIVGDMKLRQACLPL
CIIAAEIQTTLCRNFRSLKYFRLCCIF

SEQ ID NO:106

Mouse T2R01 nucleotide sequence

AGCTGTGCGTGAGCAAAGCATTTCTTGTCTGCCACTTCTGAGCTGTGTGAGGAGACACAT
TATCACGGAAAGAGATTCAGACTCTGTCGCTGTCAAACCTGTATGTTTGCTCCTCTTTTA
CTGTGAAGGCAGAGTTACGAAAAAAAATGTTATGAGAACCAACTCAGAAATTGACAAAAA
TTTTCTAAATGTCATTTTTAAAAATTATATTTCAAATGGAAATGTGAGCAAATCTTTATA
ACTAATATATAAA**ATGCAGCATCTTTTAAAGACAATATTTGTTATCTGCCATAGCACACT**
TGCAATCATTTTAATCTTTGAATTAATAATTGGAATTTTAGGAAATGGGTTCATGGCCCT
GGTGCACTGTATGGACTGGGTTAAGAGAAAGAAAATGTCCTTAGTTAATAAAATCCTCAC

TGCTTTGGCAATCTCCAGAATTTTTCATCTCAGTTTATTGCTTATAAGTTTAGTCATATT
CTTTTCATATTCTGATATTCCTATGACTTCAAGGATGACACAAGTCAGTAATAATGTTTG
GATTATAGTCAATCATTTCAGTATCTGGCTTTCTACATGCCTCAGTGTCCTTTATTTTCT
CAAGATATCCAATTTTTCTAACTCTTTTTTTCTTTATCTAAAGTGGAGAGTTGAAAAAGT
AGTTTCAGTTACACTGTTGGTGTCATTGCTCCTCCTGATTTTAAATATTTTATTAATTAA
CTTGGAAATTAGCATATGCATAAAGGAATGTCAAAGAAACATATCATGCAGCTTCAGTTC
TCATTACTATGCAAAGTGTCACAGGCAGGTGATAAGGCTTCACATTATTTTCCTGTCTGT
CCCCGTTGTTTTGTCCCTGTCAACTTTTCTCCTGCTCATCTTCTCCCTGTGGACACTTCA
CCAGAGGATGCAGCAGCATGTTCAGGGAGGCAGAGATGCCAGAACCACGGCCCACTTCAA
AGCCCTACAAACTGTGATTGCATTTTTCCTACTATATTCCATTTTTATTCTGTCTGTCTT
AATACAAATATGAATTACTGAAGAAAAATCTTTTCGTTGTATTTTGTGAGGTTGTATATA
TAGCTTTTCCGACATTCCATTCATATATTCTGATTGTAGGAGACATGAAGCTGAGACAGG
CCTGCCTGCCTCTCTGTATTATCGCAGCTGAAATTCAGACTACACTATGTAGAAATTTTA
GATCACTAAAGTACTTTAGATTATGTTGTATATTCTAGACAAAAATTAACTGATACAAAT
GTCTTTTGTATTTTTCATTTTAAATATCCTTTAATTTTGACTGCATGAAATTGATTTCTG
CTTGCAATTATCACTGATTAAAACTATTAATAATTTAACTAGTTGTATACAAGG

SEQ ID NO:107

Mouse T2R02 amino acid sequence

MESVLHNFATVLIYVEFIFGNLSNGFIVLSNFLDWVIKQKLSLIDKILLTLAISRITLIW
EIYAWFKSLYDPSSFLIGIEFQIIYFSWVLSSHFSLWLATTLSVFYLLRIANCSWQIFLY
LKWRLKQLIVGMLLGSLVFLLGNLMQSMLEERFYQYGRNTSVNTMSNDLAMWTELIFFNM
AMFSVIPFTLALISFLLLIFSLWKHLQKMQLISRRHRDPSTKAHMNALRIMVSFLLLYTM
HFLSLLISWIAQKHQSELADIIGMITELMYPSVHSCILILGNSKLKQTSLCMLRHLRCRL
KGENITIAYSNQITSFCVFCVANKSMR

SEQ ID NO:108

Mouse T2R02 nucleotide sequence

CAGCACAGTGAAAAACTCATGGGCCACTTGGTCACCCAGGGACAGGCGACGCTGTTATAT
GCCAAGCTTTCTATGAAC**ATGGAATCTGTCCTTCACAACTTTGCCACTGTACTAATATAC**

GTGGAGTTTATTTTTGGGAATTTGAGCAATGGATTCATAGTGTTGTCAAACTTCTTGGAC
TGGGTCATTAAACAAAAGCTTTCCTTAATAGATAAAATTCTTCTTACATTGGCAATTTCA
AGAATCACTCTCATCTGGGAAATATATGCTTGGTTTAAAAGTTTATATGATCCATCTTCC
TTTTTAATTGGAATAGAATTTCAAATTATTTATTTTAGCTGGGTCCTTTCTAGTCACTTC
AGCCTCTGGCTTGCCACAACTCTCAGCGTCTTTTATTTACTCAGAATAGCTAACTGCTCC
TGGCAGATCTTTCTCTATTTGAAATGGAGACTTAAACAACTGATTGTGGGGATGTTGCTG
GGAAGCTTGGTGTTCTTGCTTGGAAATCTGATGCAAAGCATGCTTGAAGAGAGGTTCTAT
CAATATGGAAGGAACACAAGTGTGAATACCATGAGCAATGACCTTGCAATGTGGACCGAG
CTGATCTTTTTCAACATGGCTATGTTCTCTGTAATACCATTTACATTGGCCTTGATTTCT
TTTCTCCTGCTAATCTTCTCTTTGTGGAAACATCTCCAGAAGATGCAGCTCATTTCCAGA
AGACACAGAGACCCTAGCACCAAGGCCCACATGAATGCCTTGAGAATTATGGTGTCCTTC
CTCTTGCTCTATACCATGCATTTCCTGTCTCTTCTTATATCATGGATTGCTCAAAAGCAT
CAGAGTGAACTGGCTGATATTATTGGTATGATAACTGAACTCATGTATCCTTCAGTCCAT
TCATGTATCCTGATTCTAGGAAATTCTAAATTAAAGCAGACTTCTCTTTGTATGCTGAGG
CATTTGAGATGTAGGCTGAAAGGAGAGAATATCACAATTGCATATAGCAACCAAATAACT
AGCTTTTGTGTATTCTGTGTTGCAAACAAATCTATGAGGTAGTTGTTCAAGGAATCCTTC
CTTGACTTATTGTATCATGGAAGTCATATGGGGGAGTCTGAAAGAGCTGTCTTCTGTAAG
CAAGGTTTGTATACACTAGTGGGGCTGGGACACCAACCCAAGCACAAAACCTAGCTATAA
CCTATCCTGGCTGCAGGATATGCTGGAACAATGGTGGCTTGGAAATTGTGGGACTGGCAA
AGCAATAGCTAGTCTAACTTGAGGCCCATTCCACAGCAGGAAGCTCATGCCCACCTCTGC
CTGGATGGCCAGGAAGCAAAATCTTGATGGCCCCAAGACCTATGGTAAACTGAACACTAC
TGGAAAAAGAAAGACTCGTGTTAATGATCTATCAAATATTTCCTAATGATATTCTGATAA
ACTCATATATTAGTCCCTGTCCTAATCATCATCACTGGGACTCCTTCCCAGCACCTGATG
GGAGCAGATAGAGATCTACATCCAAATAGTAAGTGTATCTTGGGGAACTCCACTTAAGAA
TAGAAGGAACAATTATGAGAGCCAGAGTGATCCAGAACACTAGGATCACAGAATCAACTA
AGCAGCATGCATAGGGGTTAATGGAGACTGAAGTGGCAATCACAGAGCCTGCATAGGTCT
ACACTAAGTCCTCTGTGTATATACTGTGGCTGTTTAGCTTAGGAATTTTGTTGGACTCCT
AACAATGGATAAGGAATTC

SEQ ID NO:109

Mouse T2R03 amino acid sequence

MVLTIRAILWVTLITIISLEFIIGILGNVFIALVNIIDWVKRGKISAVDKTYMALAISRT
AFLLSLITGFLVSLLDPALLGMRTMVRLLTISWMVTNHFSVWFATCLSIFYFLKIANFSN
SIFLVLKWEAKKVVSVTLVVSVIILIMNIIVINKFTDRLQVNTLQNCSTSNTLKDYGLFL
FISTGFTLTPFAVSLTMFLLLIFSLWRHLKNMCHSATGSRDVSTVAHIKGLQTVVTFLLL
YTAFVMSLLSESLNINIQHTNLLSHFLRSIGVAFPTGHSCVLILGNSKLRQASLSVILWL
RYKYKHIENWGP

SEQ ID NO:110

Mouse T2R03 nucleotide sequence

CTTTAATAGCAGGGTGTGAATATTTAAATTTTCTTTCTGCAGCAACTACTGAGGGCTTCA
GACTGCTGTATACAGGGCATGAAGCATCTGGATGAAGTTCAGCTGTGCTGCCTTTGACAA
CAATTTTTTGTGTATGTGTGGAGAACATAAACCATTTCATTAGTGAAATTTGGCTTTTGG
GTGACATTGTCTATGATAGTTCTGAAAGTGATTATGTTAAGAATCAGACACAGCCGTCTA
GAAGATTGTATTAACACATCTTTGGTAGTTCAGAAGAAATTAGATCATC**ATGGTGTTGAC**
AATAAGGGCTATTTTATGGGTAACATTGATAACTATTATAAGTCTGGAGTTTATCATAGG
AATTTTAGGAAATGTATTCATAGCTCTCGTGAACATCATAGACTGGGTTAAAAGAGGAAA
GATCTCTGCAGTGGATAAGACCTATATGGCCCTGGCCATCTCCAGGACTGCTTTTTTATT
GTCACTAATCACAGGGTTCTTGGTATCATTATTGGACCCAGCTTTATTGGGAATGAGAAC
GATGGTAAGGCTCCTTACTATTTCCTGGATGGTGACCAATCATTTCAGTGTCTGGTTTGC
AACATGCCTCAGTATCTTTTATTTTCTCAAGATAGCTAATTTCTCAAATTCTATTTTCCT
TGTTCTCAAATGGGAAGCTAAAAAAGTGGTATCAGTGACATTGGTGGTATCTGTGATAAT
CTTGATCATGAACATTATAGTCATAAACAAATTCACTGACAGACTTCAAGTAAACACACT
CCAGAACTGTAGTACAAGTAACACTTTAAAAGATTATGGGCTCTTTTTATTCATTAGCAC
TGGGTTTACACTCACCCCATTCGCTGTGTCTTTGACAATGTTTCTTCTGCTCATCTTCTC
CCTGTGGAGACATCTGAAGAATATGTGTCACAGTGCCACAGGCTCCAGAGATGTCAGCAC
AGTGGCCCACATAAAAGGCTTGCAAACTGTGGTAACCTTCCTGTTACTATATACTGCTTT
TGTTATGTCACTTCTTTCAGAGTCTTTGAATATTAACATTCAACATACAAATCTTCTTTC
TCATTTTTTACGGAGTATAGGAGTAGCTTTTCCCACAGGCCACTCCTGTGTACTGATTCT
TGGAAACAGTAAGCTGAGGCAAGCCTCTCTTTCTGTGATATTGTGGCTGAGGTATAAGTA
CAAACATATAGAGAATTGGGGCCCCTAAATCATATCAGGGATCCTTTTCCACATTCTAGA
AAAAAATCAGTTAATAAGAACAGGAATTTAGGAAGGAATCTGAAATTATGAATCTCATAG
GCCATGAACCTTCAGACAAAGGATTCATTAGAGAGATAGAGAGAGAACATTGTTATCTGT

AACTCGACAGGCAACACTGTAGATTATGAAAATAAATGTCAGTCTGTAATGGAAAGCAAA
ACATGCTATATTTTATTAATTGGTTTTGGTTTAAGGTCGGGATA

SEQ ID NO:111

Mouse T2R04 amino acid sequence

MLSALESILLSVATSEAMLGVLGNTFIVLVNYTDWVRNKKLSKINFILTGLAISRIFTIW
IITLDAYTKVFLLTMLMPSSLHECMSYIWVIINHLSVWFSTSLGIFYFLKIANFSHYIFL
WMKRRADKVFVFLIVFLIITWLASFPLAVKVIKDVKIYQSNTSWLIHLEKSELLINYVFA
NMGPISLFIVAIIACFLLTISLWRHSRQMQSIGSGFRDLNTEAHMKAMKVLIAFIILFIL
YFLGILIETLCLFLTNNKLLFIFGFTLSAMYPCCHSFILILTSRELKQDTMRALQRLKCC
ET

SEQ ID NO:112

Mouse T2R04 nucleotide sequence

CTGCAGCAGGTAAATCACACCAGATCCAGCAGAAGCCTTCTTGGAAATTGGCAGAG**ATGC**
TGAGTGCACTGGAAAGCATCCTCCTTTCTGTTGCCACTAGTGAAGCCATGCTGGGAGTTT
TAGGGAACACATTTATTGTACTTGTAAACTACACAGACTGGGTCAGGAATAAGAAACTCT
CTAAGATTAACTTTATTCTCACTGGCTTAGCAATTTCCAGGATTTTTACCATATGGATAA
TAACTTTAGATGCATATACAAAGGTTTTCCTTCTGACTATGCTTATGCCGAGCAGTCTAC
ATGAATGCATGAGTTACATATGGGTAATTATTAACCATCTGAGCGTTTGGTTTAGCACCA
GCCTCGGCATCTTTTATTTTCTGAAGATAGCAAATTTTTCCCACTACATATTTCTCTGGA
TGAAGAGAAGAGCTGATAAAGTTTTTGTCTTTCTAATTGTATTCTTAATTATAACGTGGC
TAGCTTCCTTTCCGCTAGCTGTGAAGGTCATTAAAGATGTTAAAATATATCAGAGCAACA
CATCCTGGCTGATCCACCTGGAGAAGAGTGAGTTACTTATAAACTATGTTTTTGCCAATA
TGGGGCCCATTTCCCTCTTTATTGTAGCCATAATTGCTTGTTTCTTGTTAACCATTTCCC
TTTGGAGACACAGCAGGCAGATGCAATCCATTGGATCAGGATTCAGAGATCTCAACACAG
AAGCTCACATGAAAGCCATGAAAGTTTTAATTGCATTTATCATCCTCTTTATCTTATATT
TTTTGGGTATTCTCATAGAAACATTATGCTTGTTTCTTACAAACAATAAACTTCTCTTTA
TTTTTGGCTTCACTTTGTCAGCCATGTATCCCTGTTGCCATTCCTTTATCCTAATTCTAA
CAAGCAGGGAGCTGAAGCAAGACACTATGAGGGCACTGCAGAGATTAAAATGCTGTGAGA

CTTGACAGAGAAATGAATGTTCTGGCACAGTTCAGCAGGGAATCCCTGGAGCCCTTTCCA
TTCCCACTATGTTCTCACACTGTCTTTAGTTGAATTGTTAAAAGTTTTTGAAACCTTTGG
CAACTGATTGACTGCAGCTACGCCAGTGTAAGATTTTCATAGTAAGAGCAAACATTGAAA
ATAAGACTTCTCAGTCTTATTTCATTGAGTTTCTAAAGCATTGACACCCATTCACCAGAA
AAACCAAAGGGGAAGAGAGGAGTTTTCAGACATGTGTGATGAATCTTGATATTTAGGACA
TGGAATTGAGGAG~CCAGAGGGATGCTACCGTGTGTCTACAGCTTTGTTTGTTAAATAGC
TACTTTTCCTTTCCCAGTTAGTTAAAGTAGATGCTTGGAGTAGTGGTGAAAATCATGGCA
GTAGATGGGATCTGTGGGAAGTGGTTGAGGAAGCAGGCTGTTTCTGAACGAAGAGACCAG
AGGACTGATTGAACTGGTCATTGTGTATATCAAAAATAGTGATTTCAGATGAAGCCAAGT
TGTAGAGCAAAGATATCTGAGGAAGAATTC

SEQ ID NO:113

Mouse T2R05 amino acid sequence

MLSAAEGILLSIATVEAGLGVLGNTFIALVNCMDWAKNNKLSM**T**GFLLIGLATSRIFIVW
LLTLDAYAKLFYPSKYFSSSLIEI**I**SYIWMTVNHLTVWFATSLSIFYFLKIANFSDCVFL
WLKRRTDKAFVFLLGCLL**T**SWVISFSFVVKVMKD**G**KVNHRNRTSEMYWEKRQFTINYVFL
NIGVISLFMMTLTACFLLIMSLWRHSRQMQSGVSGFRDLNTEAHVKAIKFLISFIILFVL
YFIGVSIEIICIFIPENKLLFIFGFTTASIYPCCHSFILILSNSQLKQAFVKV**L**QGLKFF

SEQ ID NO:114

Mouse T2R05 nucleotide sequence

ATGCTGAGTGCGGCAGAAGGCATCCTCCTTTCCATTGCAACTGTTGAAGCTGGGCTGGGA
GTTTTAGGGAACACATTTATTGCACTGGTAAACTGCATGGACTGGGCCAAGAACAATAAG
CTTTCTATGACTGGCTTCCTTCTCATCGGCTTAGCAACTTCCAGGATTTTTATTGTGTGG
CTATTAACTTTAGATGCATATGCAAAGCTATTCTATCCAAGTAAGTATTTTTCTAGTAGT
CTGATTGAAATCATCTCTTATATATGGATGACTGTGAATCACCTGACTGTCTGGTTTGCC
ACCAGCCTAAGCATCTTCTATTTCCTGAAGATAGCCAATTTTTCCGACTGTGTATTTCTC
TGGTTGAAGAGGAGAACTGATAAAGCTTTTGTTTTTCTCTTGGGGTGTTTGCTAACTTCA
TGGGTAATCTCCTTCTCATTTGTTGTGAAGGTGATGAAGGACGGTAAAGTGAATCATAGA
AACAGGACCTCGGAGATGTACTGGGAGAAAAGGCAATTCACTATTAACTACGTTTTCCTC

AATATTGGAGTCATTTCTCTCTTTATGATGACCTTAACTGCATGTTTCTTGTTAATTATG
TCACTTTGGAGACACAGCAGGCAGATGCAGTCTGGTGTTTCAGGATTCAGAGACCTCAAC
ACAGAAGCTCATGTGAAAGCCATAAAATTTTTAATTTCATTTATCATCCTTTTCGTCTTG
TATTTTATAGGTGTTTCAATAGAAATTATCTGCATATTTATACCAGAAAACAAACTGCTA
TTTATTTTTGGTTTCACAACTGCATCCATATATCCTTGCTGTCACTCATTTATTCTAATT
CTATCTAACAGCCAGCTAAAGCAAGCCTTTGTAAAGGTACTGCAAGGATTAAAGTTCTTT
TAG

SEQ ID NO:115

Mouse T2R06 amino acid sequence

MLTVAEGILLCFVTSGSVLGVLGNGFILHANYINCVRKKFSTAGFILTGLAICRIFVICI
IISDGYLKLFSPHMVASDAHIIVISYIWVIINHTSIWFATSLNLFYLLKIANFSHYIFFC
LKRRINTVFIFLLGCLFISWSIAFPQTVKIFNVKKQHRNVSWQVYLYKNEFIVSHILLNL
GVIFFFMVAIITCFLLIISLWKHNRKMQLYASRFKSLNTEVHVKVMKVLISFIILLILHF
IGILIETLSFLKYENKLLLILGLIISCMYPCCHSFILILANSQLKQASLKALKQLKCHKK
DKDVRVTW

SEQ ID NO:116

Mouse T2R06 nucleotide sequence

TATAGTTGCAGCAGAAGCAACGTTAGGGATCTGTAGAGATGCTGACTGTAGCAGAAGGAA
TCCTCCTTTGTTTTGTAACTAGTGGTTCAGTCCTGGGAGTTCTAGGAAATGGATTTATCC
TGCATGCAAACTACATTAACTGTGTCAGAAAGAAGTTCTCCACAGCTGGCTTTATTCTCA
CAGGCTTGGCTATTTGCAGAATCTTTGTCATATGTATAATAATCTCTGATGGATATTTAA
AATTGTTTTCTCCACATATGGTTGCCTCTGATGCCCACATTATAGTGATTTCTTACATAT
GGGTAATTATCAATCATACAAGTATATGGTTTGCCACCAGCCTCAACCTCTTCTATCTCC
TGAAGATAGCAAATTTTTCTCACTACATCTTCTTCTGCTTGAAGAGAAGAATCAATACAG
TATTTATCTTTCTCCTGGGATGCTTATTTATATCATGGTCAATTGCTTTCCCACAAACAG
TGAAGATATTTAATGTTAAAAAGCAGCACAGAAaTGTTTCCTGGCAGGTTTACCTCTATA
AGAATGAGTTCATtGTAAGCCACATTCTTCTCAACCTGGGAGTTATATTCTTCTTTATGG
TGGCTATCATTACATGCTTCCTATTAATTATTTCACTTTGGAAACATAACAGAAAGATGC

AGTTGTATGCCTCAAGATTCAAAAGCCTTAACACAGAAGTACATGTGAAAGTCATGAAAG
TTTTAATTTCTTTTATTATCCTGTTAATCTTGCATTTCATAGGGATTTTGATAGAAACAT
TGAGCTTTTTAAAATATGAAAATAAACTGCTACTTATTTTGGGTTTGATAATTTCATGCA
TGTATCCTTGCTGTCATTCATTTATCCTAATTCTAGCAAACAGTCAGCTGAAGCAGGCTT
CTTTGAAGGCACTGAAGCAATTAAAATGCCATAAGAAAGACAAGGACGTCAgAGTGACAT
GGTAGACTTATGGAGAAATGAATGGTCACAAGAAATAGCCTGGTGTGGAGATGTTGATAT
CTCTAAAGACCGTTTCACTTCCAAATTCTTGCAATTATTTAAAAAAAAAAGTCTTGCTGA
TATCATGGAATCATGGGAAATGTTGCAATTGTGTTTTGGGGACAGGGTGACCAGTGAAGG
TATGGTTAAGCAGCGAAACACTCATACAGCTCGTTCGTTCTTTTTGTATTTTATTTTGTG
TTGGTGGCCTTCCAAGACATGATTTCTCTATGTAAGTTTTGG

SEQ ID NO:117

Mouse T2R07 amino acid sequence

MLNSAEGILLCVVTSEAVLGVLGDTYIALFNCMDYAKNKKLSKIGFILIGLAISRIGVVW
IIILQGYIQVFFPHMLTSGNITEYITYIWVFLNHLSVWFVTNLNILYFLKIANFSNSVFL
WLKRRVNAVFIFLSGCLLTSWLLCFPQMTKILQNSKMHQRNTSWVHQRKNYFLINQSVTN
LGIFFFIIVSLITCFLLIVFLWRHVRQMHSDVSGFRDHSTKVHVKAMKFLISFMVFFILH
FVGLSIEVLCFILPQNKLLFITGLTATCLYPCGHSIIVILGNKQLKQASLKALQQLKCCE
TKGNFRVK

SEQ ID NO:118

Mouse T2R07 nucleotide sequence

TTCATAATGAAGAGGAGGCAGGGCAATGTTGGTTTCTGTTGTCTGACCAGTGTATTTGAC
AGTGATACTACACATTTGATTGCTAAATGCAAATAGTTCCAAAGGAACAAGTAAATTTTA
TGAAATAGAAGCTTCTATTTGCTTATTAACAAACTGCAAGCAAACATTAGTCTGCACACA
TTTTATAGACAAGCTAAATCTTCAAAAGCAATAAAAAAGAGCACCCATAAAGTTCTGACT
CTATCACATGACAATAGGCTTGAAAAGATTGTCTATGTAGATAAAGAAGATGGCATAACT
TCTCCATCAAGAAGCCAGTATATGGGACATTCTCCAGCAGATAATTTACAATAGATGCAG
CAGAAGTAACCTTAGAGATCTGTAAAG**ATGCTGAATTCAGCAGAAGGCATCCTCCTTTGT**
GTTGTCACTAGTGAGGCTGTGCTCGGAGTTTTAGGGGACACATATATTGCACTTTTTAAC

TGCATGGACTATGCTAAGAACAAGAAGCTCTCTAAGATCGGTTTCATTCTCATTGGCTTG
GCGATTTCCAGAATTGGTGTTGTATGGATAATAATTTTACAAGGGTATATACAAGTATTT
TTTCCACACATGCTTACCTCTGGAAACATAACTGAATATATTACTTACATATGGGTATTT
CTCAATCACTTAAGTGTCTGGTTTGTCACCAACCTCAACATCCTCTACTTTCTAAAGATA
GCTAATTTTTCCAACTCTGTATTTCTCTGGCTGAAAAGGAGAGTCAATGCAGTTTTTATC
TTTCTGTCAGGATGCTTACTTACCTCATGGTTACTATGTTTTCCACAAATGACAAAGATA
CTTCAAAATAGTAAAATGCACCAGAGAAACACATCTTGGGTCCACCAGCGGAAAAATTAC
TTTCTTATTAACCAAAGTGTGACCAATCTGGGAATCTTTTTCTTCATTATTGTATCCCTG
ATTACCTGCTTTCTGTTGATTGTTTTCCTCTGGAGACATGTCAGACAAATGCACTCAGAT
GTTTCAGGATTCAGAGACCACAGCACAAAAGTACATGTGAAAGCTATGAAATTTCTAATA
TCTTTTATGGTCTTCTTTATTCTGCATTTTGTAGGCCTTTCCATAGAAGTGCTATGCTTT
ATTCTGCCACAAAATAAACTGCTCTTTATAACTGGTTTGACAGCCACATGCCTCTATCCC
TGCGGTCACTCAATCATCGTAATTTTAGGAAATAAGCAGTTAAAGCAAGCCTCTTTGAAG
GCACTGCAGCAACTAAAATGCTGTGAGACAAAAGGAAATTTCAGAGTCAAATAAATGGGT
TTGCAAATAAATAGCTGCCTTGTTCTTcCACTGGTTTTTACCCTGTTAGTTGATGTTATG
AAAAGTTCCTGCTATGGTTGATGACATCTCAAGGAATCTATTTTTCTGGTGGCATGTTAA
GTCCACGTGAAGCCTCACTTCATACTGTGACTTGACTATGCAAATTCTTTCCACAAAATA
ACCAGATAACATTCAGCCTGGAGATAAATTCATTTAAAGGCTTTTATGGTGAGGATAAAC
AAAAAAAAAAAATCATTTTTCTGTGATTCACTGTAACTCCCAGGATGAGTAAAAGAAAAC
AAGACAAATGGTTGTGATCAGCCTTTGTGTGTCTAGACAGAGCTAGGGACCAGATGTTGA
TGCTTGTGTGTGGTTTTGAGTTCTTTAAGAAGTTATTGCCTCTCTGCCATTCGGTATTCC
TCAGGTGAGAATTC

SEQ ID NO:119

Mouse T2R08 amino acid sequence

MLWELYVFVFAASVFLNFVGIIANLFIIVIIIKTWVNSRRIASPDRILFSLAITRFLTLG
LFLLNSVYIATNTGRSVYFSTFFLLCWKFLDANSLWLVTILNSLYCVKITNFQHPVFLLL
KRTISMKTTSLLLACLLISALTTLLYYMLSQISRFPEHIIGRNDTSFDLSDGILTLVASL
VLNSLLQFMLNVTFASLLIHSLRRHIQKMQRNRTSFWNPQTEAHMGAMRLMICFLVLYIP
YSIATLLYLPSYMRKNLRAQAICMIITAAYPPGHSVLLIITHHKLKAKAKKIFCFYK

SEQ ID NO:120

Mouse T2R08 nucleotide sequence

AAGCTTGTTTGTAATTAGGCATTCCTAAGAAAATAAGAACAGGAGTGAAGAAATAGTAAT
TTAATCCTTGAAAGATTTGCATCTCAGTAAAAGCAGCTGCCTCTTAGACCAGAAATGGTG
TTTGCCATGCTGGAAAATAAAAAGGAGACCTCTTTCCAGGCTGCATCCTGTGTCTGCTTA
CTTATTTCAGTTTGTTTTCATCGGCACCAAACGAGGAAAG**ATGCTCTGGGAACTGTATGT**
ATTTGTGTTTGCTGCCTCGGTTTTTTTAAATTTTGTAGGAATCATTGCAAATCTATTTAT
TATAGTGATAATTATTAAGACTTGGGTCAACAGTCGCAGAATTGCCTCTCCGGATAGGAT
CCTGTTCAGCTTGGCCATCACTAGATTCCTGACTTTGGGGTTGTTTCTACTGAACAGTGT
CTACATTGCTACAAATACTGGAAGGTCAGTCTACTTTTCCACATTTTTTCTATTGTGTTG
GAAGTTTCTGGATGCAAACAGTCTCTGGTTAGTGACCATTCTGAACAGCTTGTATTGTGT
GAAGATTACTAATTTTCAACACCCAGTGTTTCTCCTGTTGAAACGGACTATCTCTATGAA
GACCACCAGCCTGCTGTTGGCCTGTCTTCTGATTTCAGCCCTCACCACTCTCCTATATTA
TATGCTCTCACAGATATCACGTTTTCCTGAACACATAATTGGGAGAAATGACACGTCATT
TGACCTCAGTGATGGTATCTTGACGTTAGTAGCCTCTTTGGTCCTGAACTCACTTCTACA
GTTTATGCTCAATGTGACTTTTGCTTCCTTGTTAATACATTCCTTGAGAAGACATATACA
GAAGATGCAGAGAAACAGGACCAGCTTTTGGAATCCCCAGACGGAGGCTCACATGGGTGC
TATGAGGCTGATGATCTGTTTCCTCGTGCTCTACATTCCATATTCAATTGCTACCCTGCT
CTATCTTCCTTCCTATATGAGGAAGAATCTGAGAGCCCAGGCCATTTGCATGATTATTAC
TGCTGCTTACCCTCCAGGACATTCTGTCCTCCTCATTATCACACATCATAAACTGAAAGC
TAAAGCAAAGAAGATTTTCTGTTTCTACAAGTAGCAGAATTTCATTAGTAGTTAACAGCA
TCAATTCATGGTTTGGTTGCATTAGAAATGTCTCAGTGATCTAAGGACTTAATTTTGTGA
TCTTGTATCTGGCATCCTGACCCTGAGACTAAGTGCTTATATTTTGGTCAATACAGCATC
TTTTGGCTAATATTTTAAAGTAAATCACATTCCATAAGAAATTGTTTAAGGGATTTACGT
ATTTTTCATGGCTATCACATTCCTAGACAATGGAAATCACCATACTGTTTCGCTAGCTAC
TGAAGTACCAGGGGAAAGTCCATGAATGAAGGCCACATTGTGATGTTCTTGGTTAGCACA
GATTAGAGAATTTGGCCTCAACTGAGCAAGATATC

SEQ ID NO:121

Mouse T2R09 amino acid sequence

MEHLLKRTFDITENILLIILFIELIIGLIGNGFTALVHCMDWVKRKKMSLVNKILTALAT
SRIFLLWFMLVGFPISSLYPYLVTTRLMIQFTSTLWTIANHISVWFATCLSVFYFLKIAN
FSNSPFLYLKRRVEKVVSVTLLVSLVLLFLNILLLNLFTNMCINEYHQINISYIFISYYH
LSCQIQVLGSHIIFLSVPVVLSLSTFLLLIFSLWTLHKRMQQHVQGGRDARTTAHFKALQ
AVIAFLLLYSIFILSLLLQFWIHGLRKKPPFIAFCQVVDTAFPSFHSYVLILRDRKLRHA
SLSVLSWLKCRPNYVK

SEQ ID NO:122

Mouse T2R09 nucleotide sequence

GAATTCAGAAATCATCAAAAAATCTTCAAAACTACATGTTTAAAATAGCACTTCAAATGA
ATACATTTGCAAATCTTTACAACTAATACATAAA**ATGGAGCATCTTTTGAAGAGAACATT**
TGATATCACCGAGAACATACTTCTAATTATTTTATTCATTGAATTAATAATTGGACTTAT
AGGAAACGGATTCACAGCCTTGGTGCACTGCATGGACTGGGTTAAGAGAAAAAAAATGTC
ATTAGTTAATAAAATCCTCACCGCTTTGGCAACTTCTAGAATTTTCCTGCTCTGGTTCAT
GCTAGTAGGTTTTCCAATTAGCTCACTGTACCCATATTTAGTTACTACTAGACTGATGAT
ACAGTTCACTAGTACTCTATGGACTATAGCTAACCATATTAGTGTCTGGTTTGCTACATG
CCTCAGTGTCTTTTATTTTCTCAAGATAGCCAATTTTTCTAATTCTCCTTTTCTCTATCT
AAAGAGGAGAGTTGAAAAAGTAGTTTCAGTTACATTACTGGTGTCTCTGGTCCTCTTGTT
TTTAAATATTTTACTACTTAATTTGGAAATTAACATGTGTATAAATGAATATCATCAAAT
AAACATATCATACATCTTCATTTCTTATTACCATTTAAGTTGTCAAATTCAGGTGTTAGG
AAGTCACATTATTTTCCTGTCTGTCCCCGTTGTTTTGTCCCTGTCAACTTTTCTCCTGCT
CATCTTCTCCCTGTGGACACTTCACAAGAGGATGCAGCAGCATGTTCAGGGAGGCAGAGA
TGCCAGAACCACGGCCCACTTCAAAGCCTTGCAAGCAGTGATTGCCTTTCTCCTACTATA
CTCCATTTTTATCCTGTCACTGTTACTACAATTTTGGATCCATGGATTAAGGAAGAAACC
TCCTTTCATTGCATTTTGTCAGGTTGTAGATACAGCTTTTCCTTCATTCCATTCATATGT
CTTGATTCTGAGAGACAGGAAGCTGAGACACGCCTCTCTCTCTGTGTTGTCGTGGCTGAA
ATGCAGGCCAAATTATGTGAAATAATATTTCTTTGTATTTTCATTTTCAATTTTAAAATA
TTCTTAGAATTTGACTGCATGTATTTCATCTTTTATTTGAAACAACCACTAATTAAAGCT
ATTACTAATTTAGCAAGTCGTATACAAGGTTATTTTTTAATACACATATCAAAAACTGAC
ATGTTTATGTTCTACAAAAACCTGAATATATCAAAATTATATAAATTTTGTATCAACGAT
TAACAATGGAGTTTTTTTATTTATGACCTGTCACGGGACTCCGGTGGAGTCAGCTTGTCA
GATGAAAGTCTGAAAGCTT

SEQ ID NO:123

Mouse T2R10 amino acid sequence

MFSQIISTSDIFTFTIILFVELVIGILGNGFIALVNIMDWTKRRSISSADQILTALAITR
FLYVWFMIICILLFMLCPHLLTRSEIVTSIGIIWIVNNHFSVWLATCLGVFYFLKIANFS
NSLFLYLKWRVKKVVLMIIQVSMIFLILNLLSLSMYDQFSIDVYEGNTSYNLGDSTPFPT
ISLFINSSKVFVITNSSHIFLPINSLFMLIPFTVSLVAFLMLIFSLWKHHKKMQVNAKPP
RDASTMAHIKALQTGFSFLLLYAVYLLFIVIGMLSLRLIGGKLILLFDHISGIGFPISHS
FVLILGNNKLRQASLSVLHCLRCRSKDMDTMGP

SEQ ID NO:124

Mouse T2R10 nucleotide sequence

GAATTCAACATCTTATTCAACTTCAGAAAACTGGATATTAGACACAGTGTCTGGATGAAG
CAGAGGTGATCTCTTTGGGAAAAAAAGCCAAGTAGTCATAAAGAATTTATGAAACAATTC
CTGGGATTGTTTATATTTGTTACAAACAAATTTATATGTTTGTTAGTCAGTAATGTATAA
GTGGGATTTTAAAGCATGATTATCTTGAATTTTTAACAAAAAACATGTAGTGCTTTTTAA
ATGTAGCAGAAACATTAAAAATTGAAGC**ATGTTCTCACAGATAATAAGCACCAGTGATAT**
TTTTACTTTTACAATAATATTATTTGTGGAATTAGTAATAGGAATTTTAGGAAATGGATT
CATAGCACTAGTGAATATCATGGACTGGACCAAGAGAAGAAGCATTTCATCAGCGGATCA
GATTCTCACTGCTTTGGCCATTACCAGATTTCTCTATGTGTGGTTTATGATCATTTGTAT
ATTGTTATTCATGCTGTGCCCACATTTGCTTACAAGATCAGAAATAGTAACATCAATTGG
TATTATTTGGATAGTGAATAACCATTTCAGCGTTTGGCTTGCCACATGCCTCGGTGTCTT
TTATTTTCTGAAGATAGCCAATTTTTCTAACTCTTTGTTTCTTTACCTAAAGTGGAGAGT
TAAAAAAGTAGTTTTAATGATAATACAGGTATCAATGATTTTCTTGATTTTAAACCTGTT
ATCTCTAAGCATGTATGATCAGTTCTCAATTGATGTTTATGAAGGAAATACATCTTATAA
TTTAGGGGATTCAACCCCATTTCCCACAATTTCCTTATTCATCAATTCATCAAAAGTTTT
CGTAATCACCAACTCATCCCATATTTTCTTACCCATCAACTCCCTGTTCATGCTCATACC
CTTCACAGTGTCCCTGGTAGCCTTTCTCATGCTCATCTTCTCACTGTGGAAGCATCACAA
AAAGATGCAGGTCAATGCCAAACCACCTAGAGATGCCAGCACCATGGCCCACATTAAAGC
CTTGCAAACAGGGTTCTCCTTCCTGCTGCTGTATGCAGTATACTTACTTTTTATTGTCAT

AGGAATGTTGAGCCTTAGGTTGATAGGAGGAAAATTAATACTTTTATTTGACCACATTTC
TGGAATAGGTTTTCCTATAAGCCACTCATTTGTGCTGATTCTGGGAAATAACAAGCTGAG
ACAAGCCAGTCTTTCAGTGTTGCATTGTCTGAGGTGCCAATCCAAAGATATGGACACCAT
GGGTCCATAAAAAATTTCAGAGGTCATTGGGAAACATTTTGAGATCTTATAGGGGAAAAA
GAAAATGTGGGGCTTCAAAGCTGGTAGGAGTAATATAGAGAAGGATAGGAG

SEQ ID NO:125

Mouse T2R11 amino acid sequence

MEHPLRRTFDFSQSILLTILFIELIIGLIRNGLMVLVHCIDWVKRKKFHLLIKSSPLWQT
SRICLLWFMLIHLLITLLYADLASTRTMMQFASNPWTISNHISIWLATCLGVFYFLKIAN
FSNSTFLYLKWRVQFLLLNILLVKFEINMWINEYHQINIPYSFISYYQXCQIQVLSLHII
FLSVPFILSLSTFLLLIFSLWTLHQRMQQHVQGYRDASTMAHFKALQAVIAFLLIHSIFI
LSLLLQLWKHELRKKPPFVVFCQVAYIAFPSSHSYVFILGDRKLRQACLSVLWRLKCRPN
YVG

SEQ ID NO:126

Mouse T2R11 nucleotide sequence

AATAATGTATGTGGAAGAGTTAAGTATAAATGTTGTATGAGAATGAACTCAGAAATCATC
AAAAATCTTTAAAACTGCATGTTAAAAATCACACTTCAAATGAATATATTTGTAATTCTT
TAGAACTAATAAATAAAATGGAGCATCCTTTGAGGAGAACATTTGATTTCTCCCAGAGCA
TACTTCTAACCATTTTATTCATTGAATTAATAATTGGACTTATAAGAAATGGATTAATGG
TATTGGTGCACTGCATAGATTGGGTTAAGAGAAAAAAATTTCATTTGTTAATCAAATCCT
CACCACTTTGGCAAACTTCCAGAATTTGTCTGCTCTGGTTCATGCTAATACATCTCCTGA
TTACTTTATTGTATGCAGATTTAGCTAGTACTAGAACGATGATGCAATTCGCTAGCAATC
CATGGACTATATCTAACCATATCAGCATCTGGCTTGCTACATGCCTTGGTGTCTTTTATT
TTCTCAAGATAGCCAATTTTTCTAACTCTACTTTTCTCTATCTAAAATGGCGAGTTCAGT
TCCTCTTGTTAAATATTTTACTGGTTAAATTTGAGATTAACATGTGGATAAATGAATATC
ATCAAATAAACATACCATACAGCTTCATTTCTTATTACCAAATTGTCAAATACAGGTGTT
AAGTCTTCACATTATTTTCCTGTCTGTCCCCTTTATTTTGTCCCTGTCAACTTTTCTCCT
GCTCATCTTCTCCCTGTGGACACTTCACCAGAGGATGCAGCAGCATGTTCAAGGATACAG

AGATGCCAGCACAATGGCCCACTTCAAAGCCTTGCAAGCAGTGATTGCCTTTCTCTTAAT
ACACTCCATTTTTATCCTGTCACTGTTACTACAACTTTGGAAACATGAATTAAGGAAGAA
ACCTCCTTTTGTTGTATTTTGTCAGGTTGCATATATAGCTTTTCCTTCATCCCATTCATA
TGTCTTCATTCTGGGAGACAGAAAGCTGAGACAGGCTTGTCTCTCTGTGTTGTGGAGGCT
GAAATGCAGGCCAAATTATGTGGGATAAAATCTCTTTGTGCTTTCATTTCCAATTCTTAA
ATATTCTTTGATTTTGACTGCATAAATT

SEQ ID NO:127

Mouse T2R12 amino acid sequence

GAIVNVDFLIGNVGNGFIVVANIMDLVKRRKLSSVDQLLTALAVSRITLLWYLYIMKRTF
LVDPNIGAIMQSTRLTNVIWIISNHFSIWLATTLSIFYFLKIANFSNSIFCYLRWRFEKV
ILMALLVSLVLLFIDILVTNMYINIWTDEF

SEQ ID NO:128

Mouse T2R12 nucleotide sequence

TTTTCAGCAGTGACTTTGGGAAGCAGAACGTCCTCTTAGAGACAGTGGGTGCTGCTATCC
TAGTTAATGTGGAGCAATAGTTAATGTGGATTTCCTAATTGGAAATGTTGGGAATGGATT
CATTGTTGTGGCAAACATAATGGACTTGGTCAAGAGAAGAAAGCTTTCTTCAGTGGATCA
GCTGCTCACTGCACTGGCCGTCTCCAGAATCACTTTGCTGTGGTACCTGTACATAATGAA
ACGAACATTTTTAGTGGATCCAAACATTGGTGCAATTATGCAATCAACAAGACTGACTAA
TGTTATCTGGATAATTTCTAACCATTTTAGTATATGGCTGGCCACCACCCTCAGCATCTT
TTATTTTCTCAAGATAGCAAATTTTTCTAACTCTATTTTCTGTTACCTGAGGTGGAGATT
TGAAAAGGTGATTTTGATGGCATTGCTGGTGTCCCTGGTCCTCTTGTTTATAGATATTTT
AGTAACAAACATGTACATTAATATTTGGACTGATGAATTC

SEQ ID NO:129

Mouse T2R13 amino acid sequence

MVAVLQSTLPIIFSMEFIMGTLGNGFIFLIVCIDWVQRRKISLVDQIRTALAISRIALIW
LIFLDWWVSVHYPALHETGKMLSTYLISWTVINHCNFWLTANLSILYFLKIANFSNIIFL
YLKFRSKNVVLVTLLVSLFFLFLNTVIIKIFSDVCFDSVQRNVSQIFIMYNHEQICKFLS
FTNPMFTFIPFVMSTVMFSLLIFSLWRHLKNMQHTAKGCRDISTTVHIRALQTIIVSVVL
YTIFFLSFFVKVWSFVSPERYLIFLFVWALGNAVFSAHPFVMILVNRRLRLASLSLIFWL
WYRFKNIEV

SEQ ID NO:130

Mouse T2R13 nucleotide sequence

AAGCTTGTTTGTGTTTGGATGAATTCTATTTATGTCTATCAATTTAAGATTTTCATATGA
ATCATTAAGAAATCTTGATAGTTGTTTGTGAGATATCACTTCTGCAATTTTTAAATGAAA
TTACACTCATATTTTGAAGGAACAATATGTTTTAAAGGAATATATTAACAAATCTTCAGC
AGTTACCTCAGAAGTTTGGGTATTGTTTTACAGAAA**ATGGTGGCAGTTCTACAGAGCACA**
CTTCCAATAATTTTCAGTATGGAATTCATAATGGGAACCTTAGGAAATGGATTCATTTTT
CTGATAGTCTGCATAGACTGGGTCCAAAGAAGAAAAATCTCTTTAGTGGATCAAATCCGC
ACTGCTCTGGCAATTAGCAGAATCGCTCTAATTTGGTTGATATTCCTAGATTGGTGGGTG
TCTGTTCATTACCCAGCATTACATGAAACTGGTAAGATGTTATCAACATATTTGATTTCC
TGGACGGTGATCAATCATTGTAACTTTTGGCTTACTGCAAACTTGAGCATCCTTTATTTT
CTCAAGATAGCCAACTTTTCTAACATTATTTTTCTTTATCTAAAGTTTAGATCTAAAAAT
GTGGTATTAGTGACCCTGTTAGTGTCTCTATTTTTCTTGTTCTTAAATACTGTAATTATA
AAAATATTTTCTGATGTGTGTTTTGATAGTGTTCAAAGAAATGTGTCTCAAATTTTCATA
ATGTATAACCATGAACAAATTTGTAAATTTCTTTCCTTTACTAACCCTATGTTCACATTC
ATACCTTTTGTTATGTCCACGGTAATGTTTTCTTTGCTCATCTTCTCCCTGTGGAGACAT
CTGAAGAATATGCAGCACACCGCCAAAGGATGCAGAGACATCAGCACCACAGTGCACATC
AGAGCCCTGCAAACCATCATTGTGTCTGTAGTGCTATACACTATTTTTTTTCTATCATTT
TTTGTTAAAGTTTGGAGTTTTGTGTCACCAGAGAGATACCTGATCTTTTTGTTTGTCTGG
GCTCTGGGAAATGCTGTTTTTTCTGCTCACCCATTTGTCATGATTTTGGTAAACAGAAGA
TTGAGATTGGCTTCTCTCTCTCTGATTTTTTGGCTCTGGTACAGGTTTAAAAATATAGAA
GTATAGGGTCCAAAGACCACCAAGGAATCATTTTCCTTATCCTAAAGAAAAATCAGGAG

SEQ ID NO:131

Mouse T2R14 amino acid sequence

MLSTMEGVLLSVSTSEAVLCIVGNTFIALVNCMDYNRNKKLSNIGFILTGLAISRICLVL
ILITEAYIKIFYPQLLSPVNIIELISYLWIIICQLNVWFATSLSIFYFLKIANFSHYIFV
WLKRRIDLVFFFLIGCLLISWLFSFPVVAKMVKDNKMLYINTSWQIHMKKSELIINYVFT
NGGVFLFFMIMLIVCFLLIISLWRHRRQMESNKLGFRDLNTEVHVRTIKVLLSFIILFIL
HFMGITINVICLLIPESNLLFMFGLTTAFIYPGCHSLILILANSRLKQCSVMILQLLKCC
ENGKELRDT

SEQ ID NO:132

Mouse T2R14 nucleotide sequence

CTGCAGGTATATACCTACCCTGAAGGCTTCATCTAGAGTAAACAAAGTAGTCTGTATAGT
CTGCCATTCCTCAGATTCTCCTCAACTTCCCACCCTCCAGTGACCTTTCTCCTTTTCTAC
AGTCAAACTATGGACCTCACAACCTGACACTTCTTCAGATGCAAAATATTCTCACAGAGA
CAAGTAAAACATACAAAACAAATACTTTAATTTGCCTATTAACAAATGGCAAGAAAAGAT
TCAGGCTTGAACATCCTGTAGACAAGCTAAGGACAGGAGCAACTGAAGGGATCTCCATGA
AGACCTTTCAGATTTCTACCAAAAGTAATTTTTAACTATATTTAAGTCTTTAAAGAAAGA
AAGTAAAGCCACTCTTTTATTGAACAGCAATAGATTGGAATCTTAAACAACTGCAACAGA
AGCCATTTTAAAGATCAACAAAGATGCTGAGCACA**ATGGAAGGTGTCCTCCTTTCAGTTT**
CAACTAGTGAGGCTGTGCTGGGCATTGTAGGGAACACATTCATTGCACTTGTAAACTGTA
TGGACTATAACAGGAACAAGAAGCTCTCTAATATTGGCTTTATTCTCACTGGCTTGGCAA
TTTCCAGAATTTGCCTTGTGTTGATCTTAATCACAGAGGCATACATAAAAATATTCTATC
CACAGTTGCTGTCTCCTGTCAACATAATTGAGCTCATCAGTTATCTATGGATAATTATCT
GTCAATTGAATGTCTGGTTTGCCACTAGTCTCAGTATTTTTTATTTCCTGAAGATAGCAA
ATTTTTCCCACTACATATTTGTCTGGTTAAAAAGAAGAATTGATTTAGTTTTTTTCTTCC
TGATAGGGTGCTTGCTTATCTCATGGCTATTTTCTTTCCCAGTTGTTGCGAAGATGGTTA
AAGATAATAAAATGCTGTATATAAACACATCTTGGCAGATCCACATGAAGAAAAGTGAGT
TAATCATTAACTATGTTTTCACCAATGGGGGAGTATTTTTATTTTTTATGATAATGTTAA
TTGTATGTTTCCTGTTAATCATTTCACTTTGGAGACATCGCAGGCAGATGGAATCAAATA
AATTAGGATTCAGAGATCTCAACACAGAAGTTCATGTGAGAACAATAAAAGTTTTATTGT
CTTTTATTATCCTTTTTATATTGCATTTCATGGGTATTACCATAAATGTAATTTGTCTGT
TAATCCCAGAAAGCAACTTGTTATTCATGTTTGGTTTGACAACTGCATTCATCTATCCCG

GCTGCCACTCACTTATCCTAATTCTAGCAAACAGTCGGCTGAAGCAGTGCTCTGTAATGA

TACTGCAACTATTAAAGTGCTGTGAGAATGGTAAAGAACTCAGAGACACATGACAGTCTG

GAACACATGCAATCTGGAATTGTCAGTGGAAAAAGTTACTGAAGATCTTTTCACTTGCAC

TATGCTCTTTTATTGATTTGGCATCATTATCAAACACTGTTGGAGCCTTGTGAACTCTTG

TTCAGAGTCTTCTGCCTCTCAAGGAATCACACTCC

SEQ ID NO:133

Mouse T2R15 amino acid sequence

MCAVLRSILTIIFILEFFIGNLGNGFIALVQCMDLRKRRTFPSADHFLTALAISRLALIW

VLFLDSFLFIQSPLLMTRNTLRLIQTAWNISNHFSIWFATSLSIFYLFKIAIFSNYLFFY

LKRRVKRVVLVILLLSMILLFFNIFLEIKHIDVWIYGTKRNITNGLSSNSFSEFSRLILI

PSLMFTLVPFGVSLIAFLLLIFSLMKHVRKMQYYTKGCKDVRTMAHTTALQTVVAFLLLY

TTFFLSLVVEVSTLEMDESLMLLFAKVTIMIFPSIHSCIFILKHNKLRQDLLSVLKWLQY

WCKREKTLDS

SEQ ID NO:134

Mouse T2R15 nucleotide sequence

AATAATAGATTTTTTAATATTCAGAATTTTTAAGTAATGTAGTATTGTTAGCAGCATAGC

TTATAGGAAAAGTTCCAAGTAATTTTGATTTTGTAATTCTGATTCCCCCAAATCAAGTAT

CAAGTTTACCTGCACAGACAAGGGAAGAAGTGGCAAAATGTGCAAATGAGAGCAACTTTA

TTTGACTGTCAGTACGTTGAAATTCAGTGTTTCCTTAATCAGTTATGGATTGACATTTAT

GTGCACAGAACCTGGAAGAATTTCAGCCAAGCTGGAGGTAAAAATCCAAAATTCTGATGA

TAAAACCAAAAGTAAATCACAGGTAAATCTTCTTTATTTTTCTTTTTTAATACTGTATAT

GGACATTTTTTAATACAGCATATTTTTTTTTTGAAATTTAGAAAAAAACCACTAAGAAAT

ATTCACCAATGGAATAGACTTTAAAGTCACTTAGAGA**ATGTGTGCTGTTCTACGTAGCAT**

ACTGACAATCATTTTCATTTTGGAGTTCTTCATTGGAAATCTGGGGAATGGATTCATAGC

TCTGGTACAATGCATGGACTTACGAAAGAGAAGAACGTTCCCTTCAGCAGATCATTTCCT

CACTGCTCTGGCCATCTCCAGGCTTGCTCTGATATGGGTTTTATTTCTAGATTCATTTCT

GTTTATACAATCCCCATTACTGATGACTAGAAATACATTAAGACTGATTCAGACTGCCTG

GAATATAAGCAATCATTTCAGTATATGGTTTGCTACCAGCCTCAGCATCTTTTATCTCTT

CAAGATAGCCATTTTTTCTAACTATCTTTTCTTCTACCTGAAGCGGAGAGTTAAAAGGGT
GGTTTTGGTGATACTGCTGCTATCCATGATCCTTTTGTTTTTTAATATATTTTTAGAAAT
CAAACATATTGATGTCTGGATCTATGGAACCAAAAGAAACATAACTAATGGTTTGAGTTC
AAACAGTTTTTCAGAGTTTTCCAGGCTTATTTTAATTCCAAGTTTAATGTTCACATTAGT
ACCCTTTGGTGTATCCTTGATAGCTTTCCTCCTCCTAATCTTTTCCCTTATGAAACATGT
AAGGAAGATGCAGTACTACACCAAAGGATGCAAAGATGTCAGAACCATGGCCCACACCAC
AGCCCTGCAGACTGTGGTTGCCTTCCTCCTATTATATACTACTTTCTTTCTGTCTCTAGT
TGTGGAAGTTTCAACACTTGAAATGGATGAAAGTCTGATGCTTCTGTTTGCAAAAGTTAC
TATAATGATTTTTCCTTCCATCCACTCCTGTATTTTCATTTTGAAACATAATAAGTTGAG
ACAGGACTTGCTTTCAGTACTGAAGTGGCTACAGTATTGGTGCAAGCGTGAGAAAACCTT
GGATTCATAGACCATTGTATGCATCACCTTGAATATTCTAGAGGGGTGTAGGTTCATATG
AAAGTATTGAATTTTTAAATTTGAGCCTTTTGTATATTTTCT

SEQ ID NO:135

Mouse T2R16 amino acid sequence

MNGVLQVTFIVILSVEFIIGIFGNGFIAVVNIKDLVKGRKISSVDQILTALAISRIALLW
LILVSWWIFVLYPGQWMTDRRVSIMHSIWTTFNQSSLWFATSLSIFYFFKIANFSNPIFL
YLKVRLKKVMIGTLIMSLILFCLNIIIMNAPENILITEYNVSMSYSLILNNTQLSMLFPF
ANTMFGFIPFAVSLVTFVLLVFSLWKHQRKMQHSAHGCRDASTKAHIRALQTLIASLLLY
SIFFLSHVMKVWSALLLERTLLLLITQVARTAFPSVHSWVLILGNAKMRKASLYVFLWLR
CRHKE

SEQ ID NO:136

Mouse T2R16 nucleotide sequence

TTTATGATGGAAAGAATAAAACCATTAGCAAGGCTTAATGGCTTGTTTGGTATTAGACCT
GTACATTGTTTATGGAACATGATATGGAGCTTTGTTTATTGAATATGCACAATATTTTAG
AAGCATGTTTCAAAGAATCTTAAGTAATTACAATAGAAATTGAAGCATCCAAGTGAAG**AT**
GAATGGTGTCCTACAGGTTACATTTATAGTCATTTTGAGTGTGGAATTTATAATTGGCAT
CTTTGGCAATGGATTCATAGCGGTGGTGAACATAAAGGACTTGGTCAAGGGAAGGAAGAT
CTCTTCAGTGGATCAGATCCTCACTGCTCTGGCCATCTCCAGAATTGCACTGCTGTGGTT

AATATTAGTAAGTTGGTGGATATTTGTGCTTTACCCAGGACAATGGATGACTGATAGAAG
AGTTAGCATAATGCACAGTATATGGACAACATTCAACCAGAGTAGTCTCTGGTTTGCTAC
AAGTCTCAGCATCTTTTATTTTTTCAAGATAGCAAATTTTTCCAACCCTATTTTTCTTTA
TTTAAAGGTCAGACTTAAAAAAGTCATGATAGGGACATTGATAATGTCTTTGATTCTCTT
TTGTTTAAATATTATCATTATGAATGCACCTGAGAACATTTTAATCACTGAATATAATGT
ATCTATGTCTTACAGCTTGATTTTGAATAACACACAGCTTTCTATGCTGTTTCCATTTGC
CAACACCATGTTTGGGTTCATACCTTTTGCTGTGTCACTGGTCACTTTTGTCCTTCTTGT
TTTCTCCCTGTGGAAACATCAGAGAAAGATGCAACACAGTGCCCATGGATGCAGAGATGC
CAGCACTAAGGCCCACATCAGAGCCTTGCAGACATTGATTGCCTCCCTCCTCCTGTATTC
CATTTTCTTCCTGTCTCATGTTATGAAGGTTTGGAGTGCTCTGCTTCTGGAGAGGACACT
CCTGCTTTTGATCACACAGGTTGCAAGAACAGCTTTTCCGTCAGTGCACTCCTGGGTCCT
GATTCTGGGCAATGCTAAGATGAGAAAGGCTTCTCTCTATGTATTCCTGTGGCTGAGGTG
CAGGCACAAAGAATGAAACCCTACAGTGTACAGACCTGGGGTATATTTATGTGGATGATC
TTACATATCTTAGAGGAAAATGGATTAAAAGAAATTCTCATATTTATAAATTTTTAGGTC
TGAATTACATAAAAATGTATATAATATTTTCAAAGTACAAGATAGTAGTTTATAACTTAC
ATGATAAATACTGTCTATGCATCTTCTAGTCTTTGTAGAATATGTAAAAACATGTT

SEQ ID NO:137

Mouse T2R17 amino acid sequence

MKHFWKILSVISQSTLSVILIVELVIGIIGNGFMVLVHCMDWVKKKKMSLVNQILTALSI
SRIFQLCLLFISLVINFSYTDLTTSSRMIQVMYNAWILANHFSIWIATCLTVLYFLKIAN
FSNSFFLYLKWRVEKVVSVTLLVSLLLLILNILLTNLETDMWTNEYQRNISCSFSSHYYA
KCHRQVLRLHIIFLSVPVVLSLSTFLLLIFSLWTHHKRMQQHVQGGRDARTTAHFKALQT
VIAFFLLYSIFILSVLIQIWKYELLKKNLFVVFCEVVYIAFPTFHSYILIVGDMKLRQAC
LPLCIIAAEIQTTLCRNFRSLKYFRLCCIF

SEQ ID NO:138

Mouse T2R17 nucleotide sequence

GAATTCTGGTCTGGCACCCCTGAGCTGTGTGAGTAGACACATTATCATGGAAAGAGATTC
AGAATCTGTCACTGTCAAAACTGCATGTTTGCTCCTCTGTTAGTGTGTTGGGGAAAGTTA

AGAAAAATACATTTTATGAGAATCAACTCAGAGGTTGTCAGAAATTGTCGAAACAGCATT
TTAAAAATTTACATCTCAACTGGATATATGAGCAAGTCTTTATAACTGATATATAAA**ATG**
AAGCACTTTTGGAAGATATTATCTGTTATCTCCCAGAGCACACTTTCAGTCATTTTAATC
GTGGAATTAGTAATTGGAATTATAGGAAATGGGTTCATGGTCCTGGTCCACTGTATGGAC
TGGGTTAAGAAAAAGAAAATGTCCCTAGTTAATCAAATTCTTACTGCTTTGTCAATCTCC
AGAATTTTTCAGCTCTGTTTATTGTTTATAAGTTTAGTAATCAACTTTTCATATACAGAT
TTAACTACAAGTTCAAGGATGATACAAGTCATGTACAATGCTTGGATTTTAGCCAACCAT
TTCAGCATCTGGATTGCTACATGCCTCACTGTCCTTTATTTTCTAAAGATAGCCAATTTT
TCTAACTCTTTTTTTCTTTATCTAAAGTGGAGAGTTGAAAAAGTAGTTTCAGTTACACTG
TTGGTGTCATTGCTCCTCCTGATTTTAAATATTTTACTAACTAACTTGGAAACCGACATG
TGGACAAATGAATATCAAAGAAACATATCATGCAGCTTCAGTTCTCATTACTATGCAAAG
TGTCACAGGCAGGTGTTAAGGCTTCACATTATTTTCCTGTCTGTCCCCGTTGTTTTGTCC
CTGTCAACTTTTCTCCTGCTCATCTTCTCCCTGTGGACACATCACAAGAGGATGCAGCAG
CATGTTCAGGGAGGCAGAGATGCCAGAACCACGGCCCACTTCAAAGCCCTACAAACTGTG
ATTGCATTTTTCCTACTATATTCCATTTTTATTCTGTCTGTCTTAATACAAATTTGGAAA
TATGAATTACTGAAGAAAAATCTTTTCGTTGTATTTTGTGAGGTTGTATATATAGCTTTT
CCGACATTCCATTCATATATTCTGATTGTAGGAGACATGAAGCTGAGACAGGCCTGCCTG
CCTCTCTGTATTATCGCAGCTGAAATTCAGACTACACTATGTAGAAATTTTAGATCACTA
AAGTACTTTAGATTATGTTGTATATTCTAGACAAAAATTAACTGATACAAATGTCTTTTG
TATTTTTCATTTTAAATATCCTTTAATTTTGACTGCATGAAATTGATTTCTGCTTGCAAT
TATCACTGATTAAAACTATTAATAATTTAACTAG

SEQ ID NO:139

Mouse T2R18 amino acid sequence

MVPTQVTIFSIIMYVLESLVIIVQSCTTVAVLFREWMHFQRLSPVETILISLGISHFCLQ
WTSMLYNFGTYSRPVLLFWKVSVVWEFMNILTFWLTSWLAVLYCVKVSSFTHPIFLWLRM
KILKLVLWLILGALIASCLSIIPSVVKYHIQMELVTLDNLPKNNSLILRLQQFEWYFSNP
LKMIGFGIPFFVFLASIILLTVSLVQHWVQMKHYSSSNSSLKAQFTVLKSLATFFTFFTS
YFLTIVISFIGTVFDKKSWFWVCEAVIYGLVCIHFTSLMMSNPALKKALKLQFWSPEPS

SEQ ID NO:140

Mouse T2R18 nucleotide sequence

GCGTGCTTCACAGAGCAGTATACTACAAAGCAAATGTCATTGCTGCCATTGTATATTTCT
CTAAAGACATTTCACATTTTATCTCCCTGTCCCATTGTGTGCAGAGCCCACACTTCAATC
AATCAATTCCTTAATTATAAGCTATTGTTTCATTATTTCATTTCCTACGTTTTTTTGCAT
TTTTACTAAAACTCCAAAGCAGACATTTTCTAATTATAATCCTACATGTAGTTAGAATTT
TAAAAATTATATACTATTTTCTTTGCACCACTGAGTTCAGTAGGTTTTGAAGGTTTATGC
TTAACAATTGAACATTTCATGTTAGATTATTCCTGCCTTCCTAATCTTGAATAATTAAAT
GTCCATCCAGGCTTAGAATTCACAGAGTCAACAGCTTTCACCTTGATTCTCTCACTATCT
ATCAATGACTAGAATCTGTCTGTCACTTTTGAAACCGCTAATTAAATAGTTGGTGCTTAT
TTAAAGGGTGCCCCATGCCAAGAGAAAATGTATTTCTTCTCTAGATGCCTTCGTCCTTTA
CAAGTTACATGCTTTACTGATGGTGAATTGGTTTTCTTCCAGTTCATCTGGGTTAAGTGA
CCTAAGAACCTAGCCATGGAAGGAGAAACAGAAGCAAATATTAACGATACAAGAACAAGT
TCCAGAACATTGGAAAGTACTTAGTAAAGGCATTGGAATTAGCAAAAGAATAGTAGCGAA
GCAAAAAATACTTCATCTCCATTGGGAGGTCAAGAAAGACTATGCAGTGTTTTTGATGCA
ACTTGTCATCTCTGAGTTAGACGATTCAGCACACACTTTTGAGATTGAACTTCAACAGGT
GGAGCCAGCAGACCTGAGCTTTAGGAATGATGGTGGAATTTCCAAGCAAAGACTTCCGTT
ACCTTTTTGATGTCCCCTAACAATTCGGTTGCAATGCTCACACCGCCCAACTGTTGAAAT
GCTTGGGAAAAGGGATTCTGAGACTGGCATTAGTATGTCATTTGACAGAATGGAAACATT
GCCCAGGGCATTAATGCACAGTAAAGGATTCACCTTTTCTAAGTGCTCAAATTTTAAATT
TGnATATTTTTAGAAGACATTATTTAAAAGAAAGGTGGAGAGGATATCCAAACAGCACCT
TGAGCAGATAAAGAGGTGAAGAAGAAAAAACAACATGCGTACATGATGGATTTCTCTTTA
TGAAAATGATCAAATGATCTTAGGATCAAGAATCCACACCTGAATGAGATTTGCTTGTAT
CCCTGTGTGAATTTGACCTAACAAGCAAAGCACAGACAAATGCTGTAGATAGGGAAATGT
CTATGTCAAATGTGTGTAAGGAGGATTTGCATCCACAAAGAAGTGCCCTCTTATACTGAG
AGTGCTAAGAACACATGTCCGTTTCATATTCGGAAAGTGGTATAGAGCTGTTGAGTCTTT
GGCTAGGAAGAGACTTCAGAGTGGAAGC**ATGGTGCCAACGCAAGTCACCATCTTCTCCAT**
CATCATGTATGTGCTTGAGTCCTTAGTAATAATTGTGCAAAGTTGCACAACGGTTGCAGT
GCTATTCAGAGAGTGGATGCACTTTCAAAGACTGTCACCGGTGGAGACGATTCTCATCAG
CCTGGGCATCTCACATTTCTGTCTACAGTGGACATCAATGCTATACAACTTTGGTACTTA
TTCTAGGCCTGTCCTTTTATTTTGGAAGGTATCAGTCGTCTGGGAGTTCATGAACATTTT
GACATTCTGGTTAACCAGTTGGCTTGCTGTCCTCTACTGTGTCAAGGTCTCTTCCTTCAC
TCACCCCATCTTCCTCTGGCTGAGGATGAAAATCTTGAAACTGGTTCTCTGGTTGATACT
GGGTGCTCTGATAGCTTCTTGTTTGTCAATCATCCCTTCTGTTGTTAAATATCACATCCA

GATGGAATTAGTCACCCTAGATAATTTACCCAAGAACAATTCTTTGATTCTAAGACTACA
ACAGTTTGAATGGTATTTTTCTAATCCTTTAAAAATGATTGGCTTTGGTATTCCTTTCTT
CGTGTTCCTGGCTTCTATCATCTTACTCACAGTCTCATTGGTCCAACACTGGGTGCAGAT
GAAACACTACAGCAGCAGCAACTCCAGCCTGAAAGCTCAGTTCACTGTTCTGAAGTCTCT
TGCTACCTTCTTCACCTTCTTCACATCCTATTTTCTGACTATAGTCATCTCCTTTATTGG
CACTGTGTTTGATAAGAAATCTTGGTTCTGGGTCTGCGAAGCTGTCATCTATGGTTTAGT
CTGTATTCACTTCACTTCACTGATGATGAGCAACCCTGCATTGAAAAAGGCACTGAAGCT
GCAGTTCTGGAGCCCAGAGCCTTCCTGAGGCAGGAAACACAGTTAAGCCTCTAGGGTAAG
GAGACTTTGCATTGGCACAGTCCCTATAGTGTAATGCAAACTTGAACACAAACTTCATCC
CTTTTCACATCCACAAATGGCTGCATCTATACATCATCACCAGTCTTCCCTGTATTCTGA
CCCATTCTCTTCCTGTCCTATCCATAGTCCCCAGGTTGGTTTTGATTTTTCTCATGATCA
CACCAACTCTGCTTAGCTTTTGCCACCACTGTAATAGTAAACATGGGGTGTTCTATATAT
TACAGTCAAAATCATTCTCACATTGTTGATTGCCTCACAAATTCATATAAATCCCCCTTC
CTGTCAGGAATTTATTGTCTGCTCACTTAATGCTCACCATATATTAAAGCCATTAATTCC
CCCTTCCTACCTTGAGTTTAAGAAGGAAAATGTCTTACCATTGCCCACAACCTATTCTGC
TGCTTCTAGACTTTTATGCAAGTGATTTATACACACACACACACACACACACACATAC
AAACAAC

SEQ ID NO:141

Mouse T2R19 amino acid sequence

MMEGHMLFFLLVVVVQFLTGVLANGLIVVVNAIDLIMWKKMAPLDLLLFCLATSRIILQL
CILFAQLGLSCLVRHTLFADNVTFVYIINELSLWFATWLGVFYCAKIATIPHPLFLWLKM
RISRLVPWLILASVVYVTVTTFIHSRETSELPKQIFISFFSKNTTRVRPAHATLLSVFVF
GLTLPFLIFTVAVLLLLSSLWNHSRQMRTMVGTREPSRHALVSAMLSILSFLILYLSHDM
VAVLICTQGLHFGSRTFAFCLLVIGMYPSLHSIVLILGNPKLKRNAKTFIVHCKCCHCAR
AWVTSRNPRLSDLPVPATHHSANKTSCSEACIMPS

SEQ ID NO:142

Mouse T2R19 nucleotide sequence

CTGCAGCCTAGAGAACTAATGCATAGGAAACTTATATTCCCACCTCCGTGACGTCACTCT
GACAGAAGTGAACTTATATTCCCACCTCCGTGACGTCACTCTGACAGAAGTGACTTGTTT
TTGTATGATGCTCCAGGATGCCTCATTAGCATTGAGGACAATCATAATTAAGTAAGGCAA
GGCATGAAGGTGGTCCTCACTAGGTACCTGGAGGCTTCTGGTTGCATGATTTACTTGTGA
TGACTCTGACACTTAAGAAGACCTGAAAAATGCAAAAGCTGTCATAAGGCACAGTTCGTT
TCTATGGTATCTCTTCCTTATTTGACTGACATTGAGTTGAGAAGGCAGCACTATAAACAA
ATGGGCCCCACCTTCCTCTTCCATTGTCTTTGGGTTGGCATCATCTCCAAAGGAACCTTG
GTCTAGTTGAAAGAAGCCAGAAATCATACATGGCTGAGACTGTGCATAACTCTATGTATC
ATTTAAAGAAGTCATTGGTTCTTCTTATTTTAAA**ATGATGGAAGGTCATATGCTCTTCTT**
CCTTCTGGTCGTGGTAGTGCAGTTTTTAACTGGGGTCTTGGCAAATGGCCTCATTGTGGT
TGTCAATGCCATCGACTTGATCATGTGGAAGAAAATGGCCCCACTGGATCTGCTTCTTTT
TTGCCTGGCGACTTCTCGGATCATTCTTCAATTGTGTATATTGTTTGCACAGCTGGGTCT
ATCCTGTTTGGTGAGACACACGTTATTTGCTGACAATGTTACCTTTGTCTACATTATAAA
CGAACTGAGTCTCTGGTTTGCCACATGGCTTGGTGTTTTCTACTGTGCCAAGATTGCTAC
CATCCCTCACCCACTCTTTCTGTGGCTGAAGATGAGGATATCCAGGTTGGTGCCATGGCT
GATCCTGGCATCTGTGGTCTATGTAACTGTTACTACTTTCATCCATAGCAGAGAGACTTC
AGAACTTCCTAAGCAAATCTTTATAAGCTTTTTTTCTAAAAATACAACTCGGGTCAGACC
AGCGCATGCCACACTACTCTCAGTCTTTGTCTTTGGGCTCACACTACCATTTCTCATCTT
CACTGTTGCTGTTCTGCTCTTGTTGTCCTCCCTGTGGAACCACAGCCGGCAGATGAGGAC
TATGGTGGGAACTAGGGAACCTAGCAGACATGCCCTCGTCAGTGCGATGCTCTCCATTCT
GTCATTCCTCATCCTCTATCTCTCCCATGACATGGTAGCTGTTCTGATCTGTACCCAAGG
CCTCCACTTTGGAAGCAGAACCTTTGCATTCTGCTTATTGGTTATTGGTATGTACCCCTC
CTTACACTCGATTGTCTTAATTTTAGGAAACCCTAAGCTGAAACGAAATGCAAAAACGTT
CATTGTCCATTGTAAGTGTTGTCATTGTGCAAGAGCTTGGGTCACCTCAAGGAACCCAAG
ACTCAGCGACTTGCCAGTGCCTGCTACTCATCACTCAGCCAACAAGACATCCTGCTCAGA
AGCCTGTATAATGCCATCTTAATTGTCCAACCTGAGGCTTAATCATTTCAAAGGGTAAAT
TGATGATCAAAGCCCAACACATGATATGACATCAAGGTCCATATCCCAGTAGTCATGTGG
AAATACCACCTTGCAAAATGATGTCATTGAGAAACCAGGGCAAATGGAGTCTAGGTCTTT
CAGTATGATTTGCTGCAG

SEQ ID NO:143

Mouse T2R20 amino acid sequence

MNLVEWIVTIIMMTEFLLGNCANVFITIVNFIDCVKRRKISSADRIITAIAIFRIGLLWA
MLTNWHSHVFTPDTDNLQMRVFGGITWAITNHFTTWLGTILSMFYLFKIANFSNSLFLHL
KRKLDNVLLVIFLGSSLFLVAYLGMVNIKKIAWMSIHEGNVTTKSKLKHVTSITNMLLFS
LINIVPFGISLNCVLLLIYSLSKHLKNMKFYGKGCQDQSTMVHIKALQTVVSFLLLYATY
SSCVIISGWSLQNAPVFLFCVTIGSFYPAGHSCILIWGNQKLKQVFLLLLRQMRC

SEQ ID NO:144

Mouse T2R20 nucleotide sequence

CTAGATGGGCTGTTTCATATAATGACTGGAACTCCCTACATGCTCCACGTCTTGAGTTCT
AAAATTTCACTAACAAATTTTTGACTGCCATAAATAATGAAGGTTTAAAGAAAGAACAAC
ATTTGAAGCAATGGACCAGAATTCCTCTTTATTTGACTCTTAGCAAATTGGAATGCAGCA
TCCTTTCAAGAGCAGCACTGAAATATACCAGTCAATGGCAGAGAGTAAAAAAGTATGCAA
TTGGAGACATTATGGTAATATAAATTTCCATTAAAAATGAGACTGCATTCACCTATTACA
ACACATTGCTATTCTGCTCAACACAGAGTTAAAAAGAAACAAGAACTCTTGTATACATTC
AGTTAGTCACAAGTATAATTATGTTCACATATTTTAAAAAAATGAATCATGATCTGTGAA
TTGAGCCTGGCTTTTTTTGTCTCTCTCTTTTTATTCTTTTCCTTTAGACAGACACA**ATGA**
ATTTGGTAGAATGGATTGTTACCATCATAATGATGACAGAATTTCTCTTAGGAAACTGTG
CCAATGTCTTCATAACCATAGTGAACTTCATCGACTGTGTGAAGAGAAGAAAGATCTCCT
CAGCTGATCGAATTATAACTGCTATTGCCATCTTCAGAATTGGTTTGTTGTGGGCAATGT
TAACGAACTGGCATTCACATGTGTTTACTCCAGACACAGACAATTTACAAATGAGAGTTT
TCGGTGGAATTACCTGGGCTATAACCAACCATTTTACCACTTGGCTGGGGACCATACTGA
GCATGTTTTATTTATTCAAGATAGCCAATTTTTCCAACAGTCTATTTCTTCATCTAAAAA
GAAAACTTGACAATGTTCTACTTGTGATTTTCCTGGGATCGTCTCTGTTTTTGGTTGCAT
ATCTTGGGATGGTGAACATCAAGAAGATTGCTTGGATGAGTATTCATGAAGGAAATGTGA
CCACAAAGAGCAAACTGAAGCATGTAACAAGCATCACAAATATGCTTCTCTTCAGCCTGA
TAAACATTGTACCATTTGGTATATCACTGAACTGTGTTCTGCTCTTAATCTATTCCCTGA
GTAAACATCTCAAGAATATGAAATTCTATGGCAAAGGATGTCAAGATCAGAGCACCATGG
TCCACATAAAGGCCTTGCAAACTGTGGTCTCTTTTCTCTTGTTATATGCCACATACTCTT
CCTGTGTCATTATATCAGGTTGGAGTTTGCAAAATGCACCAGTCTTCCTGTTTTGTGTGA
CAATTGGATCCTTCTACCCAGCAGGTCATTCTTGTATCTTGATTTGGGGAAACCAGAAAC
TTAAACAGGTCTTTCTGTTGTTGCTGAGGCAGATGAGATGCTGACTGAAAAAATGAAAGT
CCCCCTGTCTCTAG

SEQ ID NO:145

Mouse T2R21 amino acid sequence

MGSNVYGILTMVMIAEFVFGNMSNGFIVLINCIDWVRKGTLSSIGWILLFLAISRMVLIW
EMLITWIKYMKYSFSFVTGTELRGIMFTWVISNHFSLWLATILSIFYLLKIASFSKPVFL
YLKWREKKVLLIVLLGNLIFLMLNILQINKHIEHWMYQYERNITWSSRVSDFAGFSNLVL
LEMIVFSVTPFTVALVSFILLIFSLWKHLQKMHLNSRGERDPSTKAHVNALRIMVSFLLL
YATYFISFFLSLIPMAHKTRLGLMFSITVGLFYPSSHSFILILGHSNLRQASLWVMTYLK
CGQKH

SEQ ID NO:146

Mouse T2R21 nucleotide sequence

CTCTTTTGAAGACAATAGTTGTTCTACTAGCTATTGATAGCATGTTTACATTTGTCATTT
TCAAGTATGTTCAGAAACAAAGCTACATATTGTGGGGAGTATATAAAATATGAAAGCATG
CCATTCCCAGGCATCCAAGGATCCCTGTGTATTAAAAGGCAACAAAGCAGAACCAAATGT
TCTGTTTTGGACATGAGCTTCTTCCAATTCAACTGCTGAAAAATTTGGATAACTACATAT
AAAACTAAGAACACAGAGTGTCACAGAGCAGTCTCTGCTCTCCAATTCACCAGGATTAAT
ATTGACAGACCCAAAAGATGTCATTTAGGTAAATTTTGGATGAATCATATTGTTGTCACC
TTTGTGCTCTAGAACATAAGCTGATAGAATCAAATTTTCTTTAGCAGAGACAATGCAAAT
TGATATAACAGTGAAAGAGAATATATCTTTATTTGCATGTTAGCAAATGACAGCTGGATG
CACTTCATGATTTTCTGCAATCTAGTTCAGTCTTTAGAAGGATATATATATATATATATA
TATATATATATATATATATATATATATATATATATAAACCTTAGTCTTGAAAGATATCAGAA
AGAAGGATTTCACAAGAATGTACAGAGCCATTAGCAAAATTTTAATATACTCATCGACAT
TAGGTCAGTCACTACATAAGAAGGACTTGAATGAAAGCTTATCTTAGTTTTTGAGACTAC
AGGGACATTTCACCTTGCCAAATGAGAAGCAGTGAGTCTTCTTTGTCTGGAC**ATGGGAAG**
CAATGTGTATGGTATCTTAACTATGGTTATGATTGCAGAGTTTGTATTTGGAAATATGAG
CAATGGATTCATAGTGCTGATAAACTGCATTGATTGGGTCAGGAAAGGAACTCTTTCTTC
CATTGGTTGGATCCTGCTTTTCTTGGCCATTTCAAGAATGGTGTTGATATGGGAAATGTT
AATAACATGGATAAAATATATGAAGTATTCATTTTCATTTGTGACTGGAACAGAATTACG
GGGTATCATGTTTACCTGGGTAATTTCCAATCACTTCAGTCTCTGGCTTGCCACTATTCT

CAGCATCTTTTATTTGCTCAAAATAGCCAGTTTCTCCAAACCGGTTTTTCTCTATTTGAA
GTGGAGAGAGAAGAAAGTGCTTCTGATTGTCCTTCTGGGAAATTTGATCTTCTTGATGCT
CAACATATTACAAATAAACAAACATATAGAACACTGGATGTATCAATATGAGAGAAATAT
AACTTGGAGTTCTAGAGTGAGTGACTTTGCAGGGTTTTCAAATCTGGTCTTATTGGAGAT
GATTGTGTTCTCTGTAACACCATTCACAGTGGCCCTGGTCTCCTTCATCCTGTTAATCTT
CTCCTTGTGGAAACATCTACAGAAAATGCATCTCAATTCTAGAGGGGAACGAGACCCCAG
CACTAAAGCCCATGTGAATGCCTTGAGAATTATGGTCTCCTTCCTCTTACTCTATGCCAC
TTACTTCATATCTTTTTTTCTATCATTGATTCCCATGGCACATAAAACACGACTGGGTCT
TATGTTTAGCATAACTGTTGGGCTTTTCTACCCTTCAAGCCACTCATTTATCTTAATTTT
GGGACATTCTAATTTAAGGCAAGCCAGTCTTTGGGTGATGACATATCTTAAATGTGGGCA
AAAGCATTAGAATTTCACTATTCCATAAGGCAGCCAAACCACGTGCTACTAGGTATATGA
TACTACTCAGTGGTAAAGCCCTAGGCAAACATTAACCTTAGAAAATATATAATTTTGTGA
CTCTTCTGTATTTGATAAATCACTCACATATTTAGAAGAATGCTACAGTAGTGTGATCTT
GTACATGATTGTAACAATTCAATTTTATTAATATAGTTCAGGCATGATAACATACCCCTG
ATAACTGAAAAGTAAGTAGGATGCTACATATATATTTAGATCTAGACTTAGGGGCAAAGA
GAGACCCAGCTGATAGCTGTGCAATAAAGATTTTAATTTTCATCCTGTTGTGAGTTATCT
GAAATCTATGTCACTGAAGGCATAAGCAAGATTTTCACACACTGAAACAATCTCTTATGC
TTTCTTATATTGTTTTAAAAGTAAATTAGAAAATTTAAATAAACTTAATGGCAATTGAAA
TTACAAAAGCTAAACACATGTGGTTATTAGAAATTAGACTGTATGTAGGTCCTAGGGGAT
GGCTTAGTAAAGTGCTTTGTTGCAAGCTTCAGGATATGATTCTAAATCCCTAGATTCAAT
TAAAAACCTGGCATAAATAGCCAATGTAAAATTTGTCTGTAAAATGTAACCAGTGCTAAG
AGTACCAAGACAACAAAATGTTTACTTTTAAAACCATTTATTGATATTCTTTTAAAAATA
GGTATGTATTTTACTATTTAAATAAGATTTTGTCAAAAGCTAGTCTTGACACCTTAGGTA
AACATAGGAAGGCAACAAGTTTGAAGTCAGCTACTGGGGACAGTGCTGCTAGCAGCTGAC
AGAGGCCACTGCTGACTACAGCAGATCATTTACAGGTTCAGCACTAG

SEQ ID NO:147

Mouse T2R22 amino acid sequence

MSSLLEIFFVIISVVEFIIGTLGNGFIVLINSTSWFKNQKISVIDFILTWLAISRMCVLW
TTIAGASLRKFYKTLSYSKNFKFCFDIIWTGSNYLCIACTTCISVFYLFKIANFSNSIFF
WIKQRIHAVLLAIVLGTLMYFILFLIFMKMIANNFIYKWTKLEQNTTFPVLDTLSGFLVY
HSLYNGILIFFFIVSLTSFLLLIFSLWSHLRRMKLQGIHTKDISTEAHIKAMKTMMSFLL

FFIIYYISNIMLIVASSILDNVVAQIFSYNLIFLYLSVHPFLLVLWNSKLKWTFQHVLRK
LVCHCGGYS

SEQ ID NO:148

Mouse T2R22 nucleotide sequence

AAATGAATAATTTCATGCAAAGGATACCATTAGAATATGATCACTATTTAAATTTTAGCA
AATACATATTCAAATACCAGCACAATGTTTCAAATTTAAAATATAAACATTATAAAACCC
AGCAGAGAACAAAATGATAGCCTTGATAATTGTTGGTTTGCTCAAGAAAAATGGGTGTAT
ACTTTAACATTTAATTGGGAACTCAGTTGAGAGCATACATTTAGGGTTTTACAGAGGTAT
TCATTGCCCATTTAAGATTTGGATTCACACATCTACATCAATGTGGCTGTAATCCATTTT
CCCATGATGAAATAAGGTAGAGACTGCCTATTAAACGAC**ATGTCGAGCCTACTGGAGATT**
TTCTTTGTGATCATTTCGGTTGTAGAATTCATAATAGGAACTTTGGGAAATGGATTTATT
GTCCTGATAAACAGTACTTCTTGGTTCAAGAATCAGAAAATCTCTGTAATTGATTTCATT
CTTACTTGGTTGGCCATCTCCAGAATGTGTGTTCTATGGACAACAATTGCTGGTGCCTCT
CTCAGGAAATTCTACAAGACGTTAAGTTACTCTAAGAATTTCAAATTTTGTTTTGACATT
ATCTGGACAGGATCCAACTATTTATGCATAGCCTGTACAACGTGCATCAGTGTCTTCTAC
TTGTTCAAGATTGCCAACTTTTCTAATTCCATTTTCTTCTGGATTAAACAGAGAATTCAT
GCAGTACTTCTGGCTATTGTCCTAGGCACACTCATGTATTTCATTTTATTTCTCATTTTT
ATGAAAATGATAGCTAATAATTTTATCTACAAATGGACAAAATTGGAACAAAACACAACA
TTCCCTGTTTTAGATACTCTAAGTGGTTTCTTAGTCTACCATAGCCTCTACAATGGGATT
CTCATTTTCTTTTTTATAGTGTCTCTGACCTCATTTCTTCTTTTAATCTTCTCTTTATGG
AGCCACCTTAGGAGGATGAAACTACAGGGCATACATACCAAAGACATAAGCACAGAAGCA
CACATAAAAGCTATGAAAACTATGATGTCATTCCTTTTGTTCTTCATCATATATTATATT
AGCAACATTATGCTTATTGTGGCAAGCTCCATTCTTGACAATGTGGTTGCACAAATTTTC
TCTTATAACCTAATATTTCTGTATTTATCTGTTCATCCTTTTCTTCTGGTTTTATGGAAC
AGCAAATTGAAATGGACATTCCAGCATGTATTGAGAAAGCTGGTGTGTCATTGTGGAGGT
TATTCTTGATTTCAGTAAATACACTCAATATAACTGATGGATTTCTAAGGTAAGAAAAAT
GGAACAAGGAATAAAGAGGAGAAATATATTCCTTTTCAGATCATCTGCTCTGTCATTCTG
TCCTTAGCATGCTATTAAGAATTGTTGACTAAATCCAGTCATTTTTAACATGAGGAAAGG
ATGTTTCAATCCAACTTAGAGAGGGTACAAAATAGTCCTAGGAGGCAG

SEQ ID NO:149

Mouse T2R23 amino acid sequence

MFSQKINYSHLFTFSITLYVEIVTGILGHGFIALVNIMDWVKRRRISSVDQILTALALTR
FIYVLSMLICILLFMLCPHLPRRSEMLSAMGIFWVVNSHFSIWLTTCLGVFYFLKIANFS
NSFFLYLKWRVKKVILIIILASLIFLTLHILSLGIYDQFSIAAYVGNMSYSLTDLTQFSS
TFLFSNSSNVFLITNSSHVFLPINSLFMLIPFTVSLVAFLMLIFSLWKHHKKMQVNAKQP
RDVSTMAHIKALQTVFSFLLLYAIYLLFLIIGILNLGLMEKIVILIFDHISGAVFPISHS
FVLILGNSKLRQASLSVLPCLRCQSKDMDTMGL

SEQ ID NO:150

Mouse T2R23 nucleotide sequence

AATTTTCAGCAACCAATATGTAGACTGCTTAAATGCATCAGAAACATTATAAATTGAAGC
ATGTTTTCACAGAAAATAAACTACAGCCATTTGTTTACTTTTTCAATCACCTTGTATGTG
GAAATAGTAACGGGAATCTTAGGACATGGATTCATAGCATTAGTGAACATCATGGACTGG
GTCAAAAGAAGAAGGATCTCTTCAGTGGATCAGATTCTCACTGCTTTGGCCCTTACCAGA
TTCATTTATGTCTTGTCTATGCTGATTTGCATATTGTTATTCATGCTGTGCCCACATTTG
CCTAGGAGATCAGAAATGCTTTCAGCAATGGGTATTTTCTGGGTAGTCAACAGCCATTTT
AGCATCTGGCTTACTACATGCCTCGGTGTCTTTTATTTTCTCAAGATAGCCAATTTTTCT
AACTCTTTTTTTCTTTATCTAAAGTGGAGAGTTAAAAAAGTGATTTTAATAATAATCCTG
GCATCACTGATTTTCTTGACTTTACACATTTTATCTTTAGGGATATATGATCAGTTCTCA
ATTGCTGCTTATGTAGGAAATATGTCTTATAGTTTGACAGATTTAACACAATTTTCCAGT
ACTTTCTTATTCTCCAACTCATCCAATGTTTTCTTAATCACCAACTCATCCCATGTTTTC
TTACCCATCAACTCCCTGTTCATGCTCATACCCTTCACAGTGTCCCTGGTAGCCTTTCTC
ATGCTCATCTTCTCACTGTGGAAGCATCACAAAAAGATGCAGGTCAATGCCAAACAACCT
AGAGATGTCAGTACTATGGCCCACATTAAAGCCTTGCAAACTGTGTTCTCCTTCCTGCTG
CTGTATGCCATATACTTACTTTTCCTTATCATAGGAATTTTGAACCTTGGATTGATGGAG
AAAATAGTGATACTGATATTTGACCACATTTCTGGAGCAGTTTTTCCTATAAGCCACTCA
TTTGTACTGATTCTGGGAAACAGTAAGCTGAGACAAGCCAGTCTTTCTGTGTTGCCTTGT
CTAAGGTGCCAGTCCAAAGATATGGACACCATGGGTCTCTAGTAAATTCCAGAGTACATT
TTGTAAAAATCTTGAGGATGATCAGTTCATAGAAAAAGTTACCTTATGGGGGAAAATAA
AAAGTGGGGCTTCAATCCTGGGAGTAATAATACACAGGAGGGTAGGACAGCATGAAGGAG

ACTAGCACTATATAAGTGGTCTCATACAGGATATGGGAAAGGAAAGATTTATGCAATAAA
GAGGGAGATCATATTGGAGGATGAGGAGGCATTACATATGTAAAATGACTATAAGAATGG
AATCATGCTAATCTAAAAAAATCTGTAATGCATTTCATTCAGACTATATACATATATGCC
TATATATGGATATATGGGGATATATATTCTATACATATTTTAAAAGAACCTTTCTTATAT
AG

SEQ ID NO:151

Mouse T2R24 amino acid sequence

MVPVLHSLSTIILIAEFVWGNLSNGLIVLKNCIDWINKKELSTVDQILIVLAISRISLIW
ETLIIWVKDQLISSITIEELKIIVFSFILSSHFSLWLATALSIFYLFRIPNCYWQIFLYL
KWRIKQLIVHMLLGSLVFLVANMIQITITLEERFYQYGGNTSVNSMETEFSILIELMLFN
MTMFSIIPFSLALISFLLLIFSLWKHLQKMPLNSRGDRDPSATAHRNALRILVSFLLLYT
IYFLSLLISWVAQKNQSELVHIICMITSLVYPSFHSYILILGNYKLKQTSLWVMRQLGCR
MKRQNTPTT

SEQ ID NO:152

Mouse T2R24 nucleotide sequence

CAAAGAGGAGAAATATTTAGCTACACAGTGTACCACATACAAGCCGTTCAATCAGTATAA
GGGGAGCAGTCATATAGAATTTGGGCTTTCTTTCTTTTAAT**ATGGTACCTGTTCTGCACA**
GTCTCTCCACCATCATACTAATTGCAGAGTTTGTTTGGGGAAATTTGAGCAATGGTTTGA
TAGTGTTGAAGAACTGCATTGACTGGATCAATAAAAAAGAGCTCTCCACAGTTGATCAAA
TACTCATTGTCTTGGCAATTTCAAGAATTAGTCTCATCTGGGAAACACTAATTATATGGG
TTAAAGATCAACTAATTTCATCTATTACTATTGAAGAATTAAAAATAATTGTGTTCAGCT
TTATACTATCTAGCCACTTCAGTCTCTGGCTTGCTACAGCTCTCAGCATCTTCTATTTAT
TCAGAATACCTAATTGCTACTGGCAGATCTTTCTCTACTTGAAATGGAGAATAAAGCAAC
TGATTGTCCACATGCTTCTGGGAAGCTTGGTGTTCTTGGTTGCAAATATGATACAGATAA
CCATCACTCTTGAAGAGAGGTTCTATCAATATGGAGGAAATACAAGTGTAAATTCCATGG
AGACTGAGTTCTCAATTTTGATAGAGCTGATGTTATTTAACATGACTATGTTCTCCATTA
TACCATTTTCATTGGCCTTAATTTCTTTTCTTCTGCTAATCTTCTCTTTATGGAAACATC
TCCAGAAGATGCCACTCAATTCTAGAGGAGATAGAGACCCTAGTGCTACGGCCCACAGAA

ATGCCTTGAGAATTTTGGTCTCCTTCCTCTTGCTCTATACTATATATTTCCTGTCTCTTC
TTATATCATGGGTTGCTCAGAAGAATCAAAGTGAACTGGTTCACATTATTTGTATGATAA
CTTCACTCGTGTATCCTTCATTCCACTCATATATCCTGATTCTGGGAAATTATAAATTAA
AGCAGACCTCTCTTTGGGTAATGAGGCAGCTGGGATGTAGGATGAAAAGACAGAATACAC
CAACTACATAAGGCAGCCAAACAGTCTATTGGGTTTTAGATAACAAATCTAAATCTATGA
GGAAGTAGTTCAATAACATTTTTCCCCTTGACATGGAGTAGCAGGGTTTTTTTTTATTAG
ATATTTTCTTTACTTACATTTCAAATGCTATCCCGAAAATTCCCTGTACCCTCTCCCTGT
CCTGTTCCCCTACCCACCCACTCCCACTTCTTGGCCCTGGCATTCCCCTGGAGTATCAGT
TTTTTATTAGTCAAACTATCTCACTGACTAAGGGTCATAAAACAAGTTATTTTAACACTA
ATTTCAATTAAATCAAAGGTAAAGTGTCAGCACATGCCTTTAATCACACAATTCCATCAA
ATTCAGCACTCAGGAGAGGGTGATCTCTGTGAATTCCAGCACACTGGCGGCCGTTACTAG
TGGATCCGAGCTCGGTACCAAGCTT

SEQ ID NO:153

Mouse T2R25 amino acid sequence

MMGIAIDILWAAIIIVQFIIGNIANGFIALVNIIDWVKRRKISLMDKIITALAISRIYLL
WSTFLITLTSSLDPDIKMAVKIIRISNNTWIIANHFSIWFATCLSIFYFLKIANFSNYIF
LYLRWRFKKVVSVTLLISLIFLLLNILLMNMHIDIWSDKSKRNLSFSVRSNNCTQFPRLV
LLINTMFTSIPFTVSLLAFLLLIFSLWRHLKTMQYYAKGSEDTTTAAHIKALHMVVAFLL
FYTVFFLSLAIQYWTSGSQENNNLFYATIVITFPSVHSCILILRNSQLRQASLLVLWWLL
CKSKDVRMLVP

SEQ ID NO:154

Mouse T2R25 nucleotide sequence

AAAACTATTCGAATTGAACACAGTAACCAATTCTTCAGCGGACTTACACAAATCAAGCTA
TTATCTTATGG**ATGATGGGTATTGCCATAGATATCTTATGGGCAGCTATTATCATTGTGC**
AATTCATAATTGGGAATATTGCAAATGGATTCATAGCATTGGTGAACATCATAGACTGGG
TGAAGAGAAGAAAAATCTCTTTAATGGATAAGATCATTACTGCTTTGGCAATCTCTAGGA
TTTATCTGCTGTGGTCTACATTCTTAATTACACTAACATCTTCACTGGATCCAGATATTA
AAATGGCTGTGAAAATCATTAGAATAAGCAATAACACCTGGATTATTGCAAATCATTTCA

GCATTTGGTTTGCTACATGTCTCAGCATCTTTTATTTTCTCAAGATAGCCAATTTTTCTA
ACTATATTTTTCTCTACTTAAGGTGGAGATTTAAGAAGGTGGTTTCAGTGACATTGCTAA
TCTCTCTTATCTTCCTGCTTTTAAATATTTTACTGATGAACATGCATATTGATATCTGGA
GTGATAAGTCCAAAAGAAACCTTTCTTTTAGTGTCAGATCAAATAATTGCACTCAGTTTC
CCAGACTTGTCCTTTTAATCAACACAATGTTCACATCAATCCCCTTCACTGTGTCCCTGT
TGGCTTTTCTGCTTCTCATCTTCTCCCTGTGGAGACACCTGAAAACCATGCAATACTATG
CTAAAGGCTCCGAAGACACCACCACAGCTGCACATATAAAGGCCTTGCACATGGTAGTGG
CCTTTCTCCTGTTCTACACAGTTTTCTTTTTGTCTCTTGCCATACAATATTGGACCTCTG
GGTCTCAAGAGAATAACAACCTGTTTTATGCCACAATTGTAATTACTTTCCCTTCAGTCC
ATTCATGTATCCTGATTCTGAGAAACAGCCAGCTGAGGCAGGCATCTCTGTTGGTGCTGT
GGTGGCTGCTGTGCAAGTCCAAAGATGTACGGATGTTGGTTCCCTGAAATACTCTGTCAA
TGCTCTTTAGTAGTGAAGAAGAAAATAGCTTAGTTAAGGAAATTCTTGTTCATTACCGAA
GTATACTTTCAAGTTTATGTATC

SEQ ID NO:155

Mouse T2R26 amino acid sequence

MLPTLSVFFMLTFVLLCFLGILANGFIVLMLSREWLLRGRLLPSDMILFSLGTSRFFQQC
VGLVNSFYYFLHLVEYSGSLARQLISLHWDFLNSATFWFCTWLSVLFCIKIANFSHPAFL
WLKWRFPALVPWFLLGSILVSVIVTLLFFWGNHTIYQAFLRRKFTGNTTFKEWNRRLEID
YFMPLKVVTMSIPCSLFLVSILLLISSLRRHSLRMQHNTHSLQDPNVQAHSRALKSLISF
LVLYAVSFVSMIIDATVFISSDNVWYWPWQIILYFCMSVHPFILITNNLRFRGTFRQLLL
LARGFWVA

SEQ ID NO:156

Mouse T2R26 nucleotide sequence

GAATTCTAGACAAGGAAAGACACACACTAAATGACTTTACTTGTGGGACCTAAAATAACC
AAAATAAGTCAAAATCACAGTGATGTTACTAGGGATCTAGGATAAGGGAATGAAGAGAAA
GATGTTGGTCATAGAGTACAAAAATTCAGCTAAGAACTCAGTCCTGGAGGCTGAATGTAT
AGCTGTGTGACAGACAGCAGCTAGCCATACCAGAGTATACACTTGCCTCTTGCTGAAAGA
GTAGATCTTATGTGTCCTTGTCACACATAAAAGTAATTGAAAAAGTAACTCTCTGAGATG

ACAGATACGTTAAAATGGTTTTACTTTTCAACCTGCTCCAGTAGGGGTCCCTTTAATGTT
TGTGCTAGTAGATGGGGGACTCTCAAGTATCTTTGTGGTAGACAAATCTAAGGTGGCCTT
CATGAATACCAACCCAGACTTTTGTGACTTTGTGATCCCCCACTTTTGAAGTGGATAAGA
GCTGTGACTTGAGTCTAATCAAAGGAGTCCAACGTGTTGTTTATTCTGTAACAGTGCTTT
GTGTTTCTAGTTAATAACACAGGCAAAGAAGGCTAGGGTGACATTCCTAGGATTGTGTTA
TTTCTATCTTGCTCATGCCTCCCTCTGCTGGTCTAATGAAATAAGTCAGTGGCCATATTT
AAATATGACTACGTGGCAAATACTGATGATAGCCTGTGTGTTCCAACAAATATCCAGTAG
GAGACCTAGGCATTCAGTCCTGCAGCCACAAGGAAATAGGTTCTTTCACTGGAAAAAGAG
CAGTTTAGATGGTTATAAATTACTTAATCCATAGAAGCCATAGGGGCTTTATGTAGAGAT
TTGGGTAGAGAGGTAGACCTAGATATTGACTTAGGAGTGGCTATTCCTGAGTGGGGGTAG
ATATATGGCAGGGAAACTCAGATAAGAAAGACTTCTTTAGTGTCACGATTTTTCCTAGGT
ATCTCCTTGTGCCAGATATCTATGCGTCTATGTACCTACCTACCTACCTACCTACCTACC
TACCTACCTACCTACTGACACCTAATAGGAAGAGGCAAGTGGTCACAACCTGCAATGATG
GGATAAGAATGATGGAACTCAGTTACCAAGATTAAAATACCTTCCCCACTGATGTTATTG
CAAGCATGGCAGCATGTAGGCAAAATCAGAGAAGGCAAATCATGAGCAGCTGCTGCCCCA
TGGTACCCGAGCCCGGGAAATATTTGCATCATATCTGAGCCAAAAGCACACCTTTTATCT
ACTGCCTGAGCATTTTTCACATTGAAGTTCTGGCTCACATGCAGAATCCAACCATTTATC
TCCTGTCTCCAGAAGGGAGTGTCAGGGACTGTGGGTAGGGGCAGGGAGGAGGCCAGGAAC
CAAGGCAATCAGTGGTGACAGGAGGAGGGACTGAA**ATGCTACCAACATTATCAGTTTTCT**
TCATGTTGACCTTTGTTCTGCTCTGTTTCCTGGGGATCCTGGCCAACGGCTTCATTGTGC
TGATGCTGAGCAGGGAATGGCTACTGCGTGGTAGGCTGCTCCCCTCGGACATGATCCTCT
TCAGTTTGGGCACCTCCCGATTCTTCCAGCAGTGTGTGGGATTGGTCAACAGTTTCTATT
ACTTCCTCCATCTGGTTGAGTACTCCGGGAGCCTTGCCCGGCAGCTCATTAGTCTTCACT
GGGACTTCTTGAACTCAGCCACTTTCTGGTTTTGTACCTGGCTCAGCGTCCTGTTCTGTA
TCAAGATTGCTAACTTCTCCCATCCTGCCTTCCTGTGGTTGAAGTGGAGATTCCCAGCGT
TGGTGCCCTGGTTCTTGTTGGGCTCTATCTTGGTGTCCGTCATTGTAACTCTGCTGTTCT
TTTGGGGAAACCACACTATATATCAGGCATTCTTAAGGAGAAAGTTTACTGGGAACACAA
CCTTTAAGGAGTGGAACAGAAGGCTGGAAATAGACTATTTCATGCCTCTGAAAGTTGTCA
CCATGTCAATTCCTTGTTCTCTTTTTCTGGTCTCAATTTTGCTGTTGATCAGTTCTCTCA
GAAGGCATTCGCTAAGAATGCAGCACAATACCCACAGCTTGCAAGACCCCAACGTCCAGG
CTCACAGCAGAGCCCTGAAGTCACTCATCTCATTCCTGGTTCTTTATGCGGTGTCCTTTG
TGTCCATGATCATTGATGCTACAGTCTTCATCTCCTCAGATAATGTGTGGTATTGGCCCT
GGCAAATTATACTTTACTTTTGCATGTCTGTACATCCATTTATCCTCATCACCAATAATC
TCAGGTTCCGCGGCACCTTCAGGCAGCTACTCCTGTTGGCCAGGGGATTCTGGGTGGCCT

AGAAGGCTTGGTCTCTTTATCTAGAGCCTTTGAAGAGACTCAGGTGAGGGTAACTTCACT
TGGAAGTGAGCTCATCTACGTGGAAATGTCTTTGTAGGCAGGCATGGGGTCATACTGTGA
GGTTCCTCATTGGGAAAGAGGAGAAGAAAATACAGAGTGTCCTTCCTTACCTTAGGATAT
TATGAAAGTGGAAATTCCGAATCCTGGACCAGTATTGATCTAAGTGCAAAGTACAATATG
TCCTGTTCCTTTCATGTCTGTTTTCCTTTTGTTACTGATTCATTCTCTAGGGAATAGTCT
TGATCAACTGAATCATCTCATCTGGCTGGCCACTGGGGAGGTAAAAGAACTTTGTGTCAC
TGCTGCATTGGGATATACATGGGTGGGAAGCAAGTGTCCCTGAGGCAGAGTAGCACTCAG
TATGAGAACCTCAAAGAGCAGGTGGCTGTGCATGCAGGGGCTGGGGCAAGGAGTCCTGAT
CACTCTTCACTGTATGGGGATTATTTGTCTCTTGCCAAAATTTGGAGACTTTGGCTTTAG
TTTTGTGAAGATGACTGGAAAAATTCTTAATGCTACCCTGTATCATTTCTCAATAATATT
TTCCTTTTCCTGCCTTTAATTTTCTCCTATCTGCAGCGCCCCTTGCTTGTTATCCGTAAA
TAAATAAATAAATAAATAAATAAGCCCAATCCTCATTTTCCTGTCTTTGGGAACCCTTTT
ACTTCCCCAGGTATACGCTACAAAGCCACTTCTGCATTGAATAAACATTATCTTTCATTC
AGAAAAAGACTTAAGAATCTCACCTTTACAAAAAAAAAAAAAAAAGAATCTCACTTATTT
TATATTCAAATTCCATTTTTAAAAAGAAAAGCACAGCATTAATTTTTCTAAATACTGTTT
ATAAAAATAACTTGCTCTAAGAATTATACAAATGTTTTGAAAGGTAACTTTGGAAAAAAA
GTGTGATTAGACATGGATGTTTGTAAGACAGAACAAAGAGCTCTTGGAAGTCCATGGCAG
CTCATTGGTCTTGCCTTCAGTAGAGCCTGTCTGAATCCTGTAACCTCTTATGCCCTTTTG
TAGCTTTTCTGCAGATC

SEQ ID NO:157

Mouse T2R27 nucleotide sequence

GAATTCGCCCTTGCGGGATCCGGGAACGGATTCATAGCACTGGTAAACTTCATGGGCTGG
ATGAAGAATAGGAAGATTGCCTCCATTGATTTAATCCTCACAAGTCTGGCCATATCCAGA
ATTTGTCTATTGTGCGTAATACTATTAGATTGTTTTATATTGGTGCTATATCCAGATGTC
TATGCCACTGGTAAAGAAATGAGAATCATTGACTTCTTCTGGACACTAACCAATCACTTA
AGTATCTGGTTTGCAACCTGCCTCAGCATTTACTATTTCTTCAAGATAGGTAATTTCTTT
CACCCACTTTTCCTATGCCTCAAGTCTAGACGCCAAGGGC

SEQ ID NO:158

Mouse T2R28 amino acid sequence

GREWLRYGRLLPLDMILISLGASRFCLQLVGTVHNFYYSAQKVEYSGGLGRQFFHLHWHF
LNSATFWFCSWLSVLFCVKIAN

SEQ ID NO:159

Mouse T2R28 nucleotide sequence

GAATTCGCCCTTGCGGGATCCGGGAACGGGTTTATTGTGCTGGTGCTGGGCAGGGAGTGG
CTGCGATATGGCAGGTTGCTGCCCTTGGATATGATCCTCATTAGCTTGGGTGCCTCCCGC
TTCTGCCTGCAGTTGGTTGGGACGGTGCACAACTTCTACTACTCTGCCCAGAAGGTCGAG
TACTCTGGGGGTCTCGGCCGACAGTTCTTCCATCTACACTGGCACTTCCTGAACTCAGCC
ACCTTCTGGTTTTGCAGCTGGCTCAGTGTCCTGTTCTGTGTGAAGATTGCTAACATCACA
CACTCCACCTTCCTGTGTCTCAAGTCTAGACGCCAAGGGCG

SEQ ID NO:160

Mouse T2R29 amino acid sequence

MDGIVQNMFTFIVIVEIIIGWIGNGFIALVNCIHWYKRRKISALNQILTALAFSRIYLLL
TVFTVIAVSTLYTHVLVTRRVVKLINFHLLFSNHFSMWLAACLGLYYFLKIAHFPNSIFV
YLKMRINQVVSGTLLMSLGLLFLNTLLINSYIDTKIDDYREHLLYDFTSNNTASFYRVIL
VINNCIFTSIPFTLSQSTFLLLIFSLWRHYKKMQQHAQRCRDVLADAHIRVLQTMVTYVL
LCAIFFLSLSMQILRSELLKNILYVRFCEIVAAVFPSGHSCVLICRDTNLRGTFLSVLSW
LKQRFTSWIPNINCRSSCIF

SEQ ID NO:161

Mouse T2R29 nucleotide sequence

AGCTTGATATTTCCTATTTGTTACTGCACAGAGTTTTTTTTAAAAATTGAGTTTGTTATG
TGGATTCAATACTCAGATAGAGCTCTTTAATTTTTTTACAGTGACCTCATGAATCATAAC
TTGCCTTACAGACA**ATGGATGGAATCGTACAGAACATGTTTACATTCATTGTAATTGTGG**
AAATAATAATAGGATGGATTGGAAATGGATTCATAGCTCTGGTGAACTGCATACACTGGT

ACAAGAGAAGAAAGATCTCTGCACTGAATCAAATACTCACAGCCTTGGCTTTCTCCAGAA
TCTACCTTCTTTTAACAGTATTCACTGTTATAGCAGTGTCTACGCTATACACACACGTGT
TGGTAACTAGAAGAGTGGTAAAACTGATTAATTTCCATTTGCTTTTCAGCAATCATTTTA
GCATGTGGCTTGCTGCATGCCTTGGCCTTTATTATTTTCTTAAAATAGCTCATTTTCCTA
ACTCTATTTTTGTTTACTTAAAGATGAGAATTAACCAGGTGGTTTCAGGGACTTTGCTCA
TGTCTTTGGGCCTCTTGTTTCTAAACACTCTGCTGATAAACTCATACATTGATACCAAGA
TAGATGACTACAGAGAACATCTACTGTATGATTTCACTTCGAATAATACTGCTTCATTTT
ACAGGGTTATTTTAGTCATTAACAACTGTATTTTCACATCTATACCCTTTACACTTTCCC
AGTCCACTTTTCTCCTGCTCATCTTCTCCCTGTGGAGACATTACAAGAAGATGCAACAGC
ATGCACAAAGATGCAGAGATGTCCTTGCAGATGCCCACATCAGAGTCTTGCAAACCATGG
TCACCTATGTCCTACTCTGTGCCATTTTCTTTCTGTCTCTTTCCATGCAAATTTTGAGGA
GTGAGTTGTTGAAGAACATTCTTTACGTTAGGTTCTGCGAGATTGTTGCAGCAGTTTTTC
CTTCAGGACACTCCTGTGTCTTAATCTGTAGAGACACAAACCTGAGAGGGACCTTTCTTT
CTGTGCTATCGTGGCTGAAGCAGAGGTTTACATCATGGATTCCTAACATAAATTGCAGAT
CATCTTGCATATTCTAAAAGAAACTGAG

SEQ ID NO:162

Mouse T2R30 amino acid sequence

MTYETDTTLMLVAVGEALVGILGNAFIALVNFMGWMKNRKIASIDLILSSVAMSRICLQC
IILLDCIILVQYPDTYNRGKEMRTVDFFWTLTNHLSVWFATCLSIFYLFKIANFFHPLFL
WIKWRIDKLILRTLLACVIISLCFSLPVTENLSDDFRRCVKTKERINSTLRCKVNKAGHA
SVKVNLNLVMLFPFSVSLVSFLLLILSLWRHTRQIQLSVTGYKDPSTTAHVKAMKAVISF
LALFVVYCLAFLIATSSYFMPESELAVIWGELIALIYPSSHSFILILGSSKLKQASVRVL
CRVKTMLKGKKY

SEQ ID NO:163

Mouse T2R30 nucleotide sequence

AAAAATGTTCATTGTTTATCTAAAATTCAAATTTAACTGAGTGCCCTACATTTTTATTTA
TTCAATCTAGTAGCTGTACTGAGGTTATTAGTGTGATTTCTGAAGCCCAAATTTGTAAAA
CTTAGCCTCAGATAAACAGCTTGAGACCATGGAAAGTAATTTGGTAAA*TTTGCATCTTAG*

CAAATAGTAGCTCAGCCTAAATTAACTGTGTGTAGAAAAGAATGACCTGCGGAGAAGATA
AATGGACATACAATATCCAGGCTAAGGATTGCCAAACACACTGTTTTTAAGACTAATTGA
GATTTAGATAAACTATCTACAGTCTTCATGTATAATTCTCATCTTCATCACAAGACAGAC
TTCAACTTAAGGAGGTAAAGACAAGGACAGCGAACCCTAAACAGCCAAGTGTAGAAACCA
AACTGCATCAAATCAGCCAGAAACTAATTGGATACTTCTCTACTTTAAA**ATGACATACGA**
AACAGATACTACCTTAATGCTTGTAGCTGTTGGTGAGGCCTTAGTAGGGATTTTAGGAAA
TGCATTCATTGCACTGGTAAACTTCATGGGCTGGATGAAGAATAGGAAGATTGCCTCTAT
TGATTTAATCCTCTCAAGTGTGGCCATGTCCAGAATTTGTCTACAGTGTATAATCCTATT
AGATTGTATTATATTGGTGCAGTATCCAGACACCTACAACAGAGGTAAAGAAATGAGGAC
CGTTGACTTCTTCTGGACACTTACCAACCATTTAAGTGTCTGGTTTGCCACCTGCCTCAG
CATTTTCTATTTATTCAAGATAGCAAACTTCTTCCACCCTCTTTTCCTCTGGATAAAGTG
GAGAATTGACAAGCTAATTCTCAGAACTCTACTGGCATGTGTGATTATCTCCCTGTGTTT
TAGCCTCCCAGTCACTGAAAATCTGAGTGATGATTTCAGACGTTGTGTTAAGACAAAGGA
GAGAATAAACTCTACTTTGAGATGCAAAGTAAATAAAGCTGGACATGCCTCTGTCAAGGT
AAATCTCAACTTGGTCATGCTGTTCCCCTTTTCTGTGTCTCTGGTCTCCTTTCTCCTCTT
GATCCTCTCCCTGTGGAGACACACCAGGCAGATACAACTCAGTGTAACAGGGTACAAAGA
TCCCAGCACAACAGCTCATGTGAAAGCCATGAAAGCAGTAATTTCCTTCCTGGCCCTGTT
TGTTGTCTACTGCCTAGCCTTTCTCATAGCCACCTCCAGCTACTTTATGCCAGAGAGTGA
ATTAGCTGTAATATGGGGTGAGCTGATAGCTCTAATCTATCCTTCAAGCCATTCATTTAT
CCTCATCCTGGGGAGTAGTAAACTAAAACAAGCATCTGTGAGGGTGCTTTGTAGAGTAAA
GACCATGTTAAAGGGAAAAAAATATTAGCATCATGAGCATATCTGAAGAAAAACTATCAC
TTTCTAAGAGAAAGGAAGACACGATCATTATCCGTCCTTTTCACATGAATATTGATTTCA
TGCAGTGACATCCTCTTAACAAACTTAAATTGAACCTTGAGAAATCTCATATACAGCAAC
TTTGCATGTCTCTATCTCTGCTTTTTCTCTCCTTTTCAATATGAGTTGACATAAAAAATA
ATTTTCAGAACAAATTATAACAGAAGAAAGGGCATTTTCATAATCAGTTCTGAATCACTC
CTCCAAATGCAAAGCTGCCTGACAAATTCAAAACAATTGTAACAGCATCTCACTGTCGTT
TGCATTCTTTGGAAAAGCAGGTGGTTTGTTCTTGGAGCCTGGCTTAGAGTTTTCTTCTTA
GACCATTGAATTATGTTCATGATTGGAGAAGAGTCAAGTACCAAGTAACAATTTTTATTG
TGAAGATGGGTGTTCATCATGTGATTTTGGCTGGCCTGGAACTTGTTATGTAGACTAGTC
TGTCATCAAACACACAAAGATCTGCCTGCCTCACCTGCCAGTTCTAGGATTCAAGGAATG
CACCACCACAGCTTGTTCAAGTGACAATTCTTACAAATGTTTTAGAAATAAATAATATAC
TAGAAATTAACACTGAATGTAAGTGCTGTTTAGGTATAAATTATGATTAAATGTTATAGT
TAGAAAATTATTTAAGATTATAGATCAGTGATGAAAATATTCTAGAATAAGTTTTATGAA
GAAACTTTTATAAAGAAACTGGAAAAAAATCTCTTGATTGCATATTGAAACAAATTTCTC

CAAAAAGAACACCTACAAATTTGCTCTAGACATCTAGACTGTATCAAACAGTGAATATGA
AAATATCATAACAGGATATAGCCTTTAGTATTGAAGACAGGTTCATCTATATTAAACCTG
CATACATACCTAAAAGACTAAGTCAATATCCCACAAACATATTTGCACTATCATGTCTAT
TGAAACACTATTCATAGTAGCTAAAATATGGCACAAAACTAGACATTCATCAATAGATGA
ATCAATAAAGCAAATGTACATACACAAGATGAAATTGTATTCAGGCATAAAGAAGAATGC
AGTCATGTCATTAGCAAAAACATAAACAGAATTGGAGGTCATTGTGATAATTGAAATAAA
CCAGACCTGGAAAAAACAAAACCTGTGTAATTTTTCTGAAGTAGAGAATATACTCTTGGA
TGGATAGATGGGTACTGTTATAGTATAAAATGTGTGTGTGTGTGTGTGTGTGTGTGTG
TATTTCATGAAAGCAAGAATGGGACTGCTTAGAGAAAGAAAAGGACAAACAGGTGAAGGG
GTGAAAGAAAAAGGCAATGACAAGGAGTAATGATATGAGCAAAGTACCATTATTAAACAT
GTGACAATATTATATAGAAACACATGATTTTGTGTGCCTACCAAAACTGGATAATAATTT
TTAAAATGTATCTATTAAAAGGAAAGAAAAGAAAGTGCAAGCCCAGGAAAGGGAGAAAAG
GAAACAATGAGAGAGAAATGGAAAATGGTGAGAAGTGAAGAGAACAAAAAGAAATGGAGT
AAGTGTGGCCAGGAATGAAGGATCTCAGCTATAGTTATCCCAGTACGGTAATACAAATCT
GTGACTCCAGCACTTGACAAGGCTGAGAGATGTGAGAGAGGGCCAGTTAACAACCAGTCT
GGGCTTATTCCAAGAGATAAGAAGATTGGGGGAAAGTATGTAGAAGGGTTTGGAGGGAAG
AGAGAGAAGAGGGAAATGATGTAATGATAGTACAAATCAAAAGTTATTTTTTCTAAAAAA
GCAATGGGACAGGAAACCAACCTAACAAGTAAAGGTGCTTGGTTCACAAGACCAGCAACC
TGAGTGCATCCTTGCTAGAATGAAATTGGCCTTACTCTGGAAAGCTTACTTCCTCAGTGT
ATTCATTGTTAAAATTCATGTGGAGATTTTAAAGAAAAAAGGAAAAAAAAAGTTAAATGG
TAGATTTGTGTAGGGGAATATTCCCCTAATTAATTGATTAGATAATAAAGATGACAAGCA
AATTGCTGTGCAAAAAGGAAGACAAGGTCTAAGAGGGGAAGAGGGGACACGGGAGGAAAA
AAAACGGCCCTTTTTAAAGCAAGGTGGGGAGTGAGGGAAGCGAGATGTAGACAGGGAACT
GTTAGACCTGGTGGCAGCTTCTGCCACCTGAAGATTTTCAACATAGTATAGTTCATGAGT
TTAGGAAGATATGTTCCCTGCCCAGCGGTTGTATCATCTGTTGATTTTAAACTAAGATTG
TCTGGTGTTTTCCATTTGCGGAGACTCAAGTAGACCAAAGGGAAAGAATGAATTC

SEQ ID NO:164

Mouse T2R31 amino acid sequence

MYMILVRAVFITGMLGNMFIGLANCSDWVKNQKITFINFIMVCLAASRISSVLMLFIDAT
IQELAPHFYYSYRLVKCSDIFWVITDQLSTWLATCLSIFYLFKVAHISHPLFLWLKWRLR
GVLVVFLVFSLFLLISYFLLLETLPIWGDIYVTLKNNLTLFSGTIKTTAFQKIIVFDIIY

LVPFLVSLASLLLLFLSLVKHSRSLDLISTTSEDSRTKIHKKAMKMLVSFLILFIIHIFF
MQLARWLLFLFPMSRPINFILTLNIFALTHSFILILGNSNLRQRAMRILQHLKSQLQELI
LSLHRFSSLY

SEQ ID NO:165

Mouse T2R31 nucleotide sequence

CTGCAGCTTTCTAGAAATCTCACCAGAATGTCTTTGTGCAGCTTTAATAGTTCCTGGTTA
TACCTTGTCACATTATAAGCTAAGACATCTTTGGTGCCACAATATACTCTCACTAATCAG
AGAGATTAGACAGAAAAATAAGTTTCTTAACAACTGTTTTAGATAGGGTCATGAAATGAC
ATAAAACACCAATGCTAAGGCAATCCATTATGTTTTCTCATGAGGAGCCCATATGTACAC
TTGAGTGTGTCTTATTATTTCCCTGAGTGATTTTGTAATTTTATTAAACACTTAACTGTG
ATTCATACTAGTTAGTTCTGAAATTCTTTTCTTCATCAAAGCCATTAATCCTGGGGTTTT
TTAAATGGAGAACCCCAAAACAAAGTGAAATGTTGTGTGTGGAGCAGGCTGTCTTCCCAC
ACACTACCATGAGATGCTCATTCTGTAATTGTTCCCCGGAATAGGAAATGCCCTGAATTC
AGGCACACAAGAGCTAGTCTGTGCACCATGTCTGGTTCTTGCATTAATACCCACTTTTGT
CACGAAGCTTCATTGATTCGCATCTTCAGAAGCTGGTATCATTATTAGTTTCTTTCCTCA
GGTGACTCTGGnCCAAAATATTAnGGCGCCCTTTAAAAAAGTAAAACTACAAAATTTCTT
TATAATTTTCTTTAAGTTTGTTATAATATAGCATGACCTACACACACACACACACACACA
CACACACACACACACACACAAGTATGCCTCTCCTTTCCTTCTAAAAATCTCACTTAAAGC
AATTGTTTAGCTGTCTTCGAAGTCTAGACTGCCACTGTCGTGCTTCTAGCCAAAACAAAT
GCAACACATAAAATGATAGAGCTCAAAACTTAGGAATCTATTTAACTGTGAAGATCACGC
AAGCAAACCTGAGAAACCTCTAGAAGGAAACCACAGCAAATCACTGGAGAGAAGGTGTTA
ATCTAGTAAGAATAGTTTTTATTTTGGGTATCCTTTTGTAGATTGGTTAGTTCATCCAAA
ATCCAACTTGTTAGTTCTTCATAAATTGTAAGTGTCTCCAACATCAAAGCACCACTTCTC
TCTTTTCCCCTGTATGAAGATGCTTTAAGTACAGAGTTACTCTTTTTCTGTACTGACAGT
AATTTAAAAAAATTGTTCACTCATTCTTTTTTGGTGTTGTTATTCTGTGTTCCTCAATGT
TATCTTTTTTTTTTCAAAACTTTCTTTTATAAAAAGTCATACACATAGCAAATGCAGTGC
ATGTTTATGGAATCCATAACTAACTTATTGAGACTTCTCCTAGTACTTTCTTTGAACAGT
AACAAAGATATCTGCTTCTACAGAGTGCAGTGTTTCAGGTGAGGAGGAACATATTATACA
AATCAGTGAAAAAAAAATCTGATTCAAATTTGTATTTTAATATATTTGACTTTATCACTT
CAGATATTACATCAATGGGAATTTTGAAGGCACACAAGTGATGATGTGGGCATAGAGACT
GTCTGTACTAGAATTTAATATTTCTTTTAAATATCTTTAAATAAAAATATGATGCTGTAT

TCATAAACAGATCTTTATAGATTAAGTATGAGATTAAAGTTGGAAAAACAAAAGACAAAA
ACCTAGGACTAAGAATTTCCTTAAGTATGTGTGAATATCAACCTAATGGAGGAAGTTTCC
AATCAAAGCTGAAATTACAGTAAAAAGGAGGAAGATAAATATGGAAAAGGATGATTTTCT
GTGGAAGTTTGTTTGAGAACTGATCCACGAGACAAATTGCTAG***AAG***TGTGGATTCCCTTT
TACTATTCAACTGCTTATAGGACTGGATCAA**ATGTATATGATACTGGTAAGAGCAGTATT**
TATAACTGGAATGCTGGGAAATATGTTCATTGGACTGGCAAACTGCTCTGACTGGGTCAA
GAACCAGAAAATCACCTTCATCAACTTCATCATGGTCTGTTTGGCAGCTTCCAGAATCAG
CTCTGTGCTGATGTTATTTATTGATGCAACCATACAAGAACTAGCGCCTCATTTCTATTA
TTCTTACCGTCTAGTAAAATGCTCTGATATATTCTGGGTTATAACTGATCAACTATCAAC
ATGGCTTGCCACCTGCCTGAGCATATTCTACTTATTCAAAGTAGCCCACATTTCCCATCC
CCTTTTCCTCTGGTTGAAGTGGAGATTGAGAGGTGTGCTTGTTGTTTTTCTTGTATTTTC
TTTGTTCTTATTGATTTCTTATTTTCTACTGCTTGAAACACTTCCTATTTGGGGAGATAT
TTATGTAACCCTTAAAAACAATCTGACCTTATTTTCAGGTACAATTAAGACCACTGCTTT
TCAAAAGATAATTGTTTTTGATATAATATATTTAGTCCCATTTCTTGTGTCCCTAGCATC
ATTGCTCCTTTTATTTTTGTCCTTGGTGAAACACTCCCGAAGCCTTGACCTGATTTCTAC
CACTTCTGAAGATTCCAGAACCAAGATTCATAAGAAGGCCATGAAAATGCTGGTGTCTTT
CCTCATTCTCTTTATAATTCACATTTTTTTCATGCAGTTAGCACGGTGGTTATTATTTTT
GTTTCCAATGAGCAGGCCAATTAATTTCATCTTAACATTAAATATCTTTGCCTTAACTCA
CTCATTTATTCTCATCCTGGGAAATAGCAATCTTCGACAGAGAGCAATGAGGATCCTGCA
ACATCTTAAAAGCCAGCTTCAAGAGCTGATCCTCTCCCTTCATAGATTCTCCAGTCTTTA
CTAGAGGAACAGCTTAACAGGGAGACTTGGAAGGTCACTGGCAAATTATTCTTCTTTGAT
TTCTTTTAAGTACTGCTGAACATATATGAACTGTCCCCAGAGCATAGTGCTATCTTATGA
GAAGGATATCATCTCACAGTCTGGTTATAAAACACAAACCAATCTTTTTATAATTTCTTT
ACAGCATTGCTAATAAAAGACTTGTAGTCTCAAATATTTTAAAGAGAATAATTAATTTTA
TAGGCAAAAGGTATGAAATTACAATTCACAGGGAAGGTTCATGACTCCTTAGATATTAAA
GTTAATTGTAAGCCACAATAGGCAGAAGATGAGCAAAATGTTGATAGGAGATAAATAAAA
TCTAAAGTTACGGAGAAAAAAAACATCAACTTGCCTTTTAGATTACTTTAAAGCTCTCTC
TCTCGCTCTCTCTCTCTGTATCTACTTACTTTATATATACAAATGTTTTGTCTGCATGTA
TTTCTTTGCACCATATAAATGTCTAAGTATCCAGAAnGTCAGCAGAGGGCATCAAATTCT
CTGGAAAGAGAGTTACAAATTGCTGTGGGTAACACTGGGTGCTGGGAACTAACCTGAGTC
CTCTGCCACAGCAACTGCTCTTCCCTGCTGAGTCATGTTTTAAGTCTCCACAACTTAAAC
TCATTGTTGATGTGGTCATTGCATAATGATGAATTTACATTCTAAGGTTTGTATCATAGG
TAGGAGGGCTGGTTTTAATCATATTCTAATGTTCTTATACAAACCCAGGTTTTGTAAGAG
ACTGTATTCTATCATGAGACTCTTTCCCCACACCGCCAATGTAACATTTTTATTAATTTT

GAGGGGAATTTTATACAGTGTACCCTGATCACCCTTGCTTCCCACTCCTTGCAGGTCTAC
CCTCCCACCATTGCTCAATCCCCCCTAAAAGAGAGAGAAACAAACCATGTCCAATTTGTG
TTGGACACATACTCAGTGGAACATGGCCAAACCCCTAGTGAGCAGTTCCTTAAAGAAAAC
TAAGCTGCCTCCCCACCACTACCACCATAGGGCATTAACTGTGAAGAGCTACACTTTAGC
TATTTTATCACCAATTTAAAAGACTGTCTTCAATAGCTTCCTCTATGGACTGTTTCTGGT
TTTAGTGGGACAGGGAGAAGGGGTCAAGAGGTTGTCACAGAAACTTTTGATGTCTCTTAT
TCTCAGTTAAAGTCCACTGCAAAAGAAGTCTGCTGGCTCTAATAAAGCTTGCAACAGCAT
GGGCCAGTGACATCATCATGATTTCTGGCAACAATATGGACCACAAATATCATGGCTCAG
GTGGCATTACGGACCACAGACATCAACATGGTCTCTGGCAGCAAGAACCAGAATCTTTTG
AGGAGGCTTCATTCAGAAAATGAATTTTTCTTCATCCCAGATATACTGATGTTGCTCAAT
CAGAGTATTAGTATGGTTGGGCACCATATTTGGGGACAGGACCTTCAATATTTCCAGGCT
GCTGTGTAACACATTATCTTTAGTGTCAGGTGCCCTTAGTGTCAGGACATGACCATCATG
TATGCGCCTGTGGGCAGAAATACATCTTTGTACTTTCTTACACCTAGCAGGGTGAGTAGC
AGGAGCAGCGGCATTAATACTTCCATACCTCTGGGCAGCCTATCAGGTATCATCTAGGCA
AGGTAAGCCCAGTAGTGGCCCAAGGCTCCTGGTGTCTACTTGGCAACAACATGCTCCTTT
GTCTGCACTGCCATATCTATGGCTGGTTCTCCATCCCTAGTTCTGCTTCTCTCAGGTTTT
ATACGACTCTATTCCACATTCTATTTTTCCAGTTCCATGAAACCAGTGTTTAAAAGTATC
ATCCCATAAGACCGGCCTTTTAAAGGTTATTCTGGAGATATTGCAGAGTCTGCAG

SEQ ID NO:166

T2R Family Consensus Sequence 1

E(F/A)(I/V/L)(V/L)G(I/V)(L/V)GN(G/T)FI(V/A)LVNC(I/M)DW

SEQ ID NO:167

T2R Family Consensus Sequence 2

(D/G)(F/L)(I/L)L(T/I)(G/A/S)LAISRI(C/G/F)L

SEQ ID NO:168

T2R Family Consensus Sequence 3

NH(L/F)(S/T/N)(L/I/V)W(F/L)(A/T)T(C/S/N)L(S/N/G)(I/V)

SEQ ID NO:169

T2R Family Consensus Sequence 4

FY(F/C)LKIA(N/S)FS(H/N)(P/S)(L/I/V)FL(W/Y)LK

SEQ ID NO:170

T2R Family Consensus Sequence 5

LLI(I/F/V)SLW(K/R)H(S/T)(K/R)(Q/K)(M/I)(Q/K)

SEQ ID NO:171

T2R Family Consensus Sequence 6

HS(F/L)(I/V)LI(L/M)(G/S/T)N(P/S/N)KL(K/R)(Q/R)

hT2R51 Full-Length cDNA (BAC AC011654) (SEQ ID NO: 172)

ATGTTGACTCTAACTCGCATCCGCACTGTGTCCTATGAAGTCAGGAGTACATTTCTGTTCA
TTTCAGTCCTGGAGTTTGCAGTGGGGTTTCTGACCAATGCCTTCGTTTTCTTGGTGAATTTT
TGGGATGTAGTGAAGAGGCAGGCACTGAGCAACAGTGATTGTGTGCTGCTGTGTCTCAGC
ATCAGCCGGCTTTTCCTGCATGGACTGCTGTTCCTGAGTGCTATCCAGCTTACCCACTTCCA
GAAGTTGAGTGAACCACTGAACCACAGCTACCAAGCCATCATCATGCTATGGATGATTGCA
AACCAAGCCAACCTCTGGCTTGCTGCCTGCCTCAGCCTGCTTTACTGCTCCAAGCTCATCC
GTTTCTCTCACACCTTCCTGATCTGCTTGGCAAGCTGGGTCTCCAGGAAGATCTCCCAGAT

GCTCCTGGGTATTATTCTTTGCTCCTGCATCTGCACTGTCCTCTGTGTTTGGTGCTTTTTTA
GCAGACCTCACTTCACAGTCACAACTGTGCTATTCATGAATAACAATACAAGGCTCAACTG
GCAGATTAAAGATCTCAATTTATTTTATTCCTTTCTCTTCTGCTATCTGTGGTCTGTGCCTC
CTTTCCTATTGTTTCTGGTTTCTTCTGGGATGCTGACTGTCTCCCTGGGAAGGCACATGAGG
ACAATGAAGGTCTATACCAGAAACTCTCGTGACCCCAGCCTGGAGGCCCACATTAAAGCCC
TCAAGTCTCTTGTCTCCTTTTTCTGCTTCTTTGTGATATCATCCTGTGTTGCCTTCATCTCTG
TGCCCCTACTGATTCTGTGGCGCGACAAAATAGGGGTGATGGTTTGTGTTGGGATAATGGC
AGCTTGTCCCTCTGGGCATGCAGCCATCCTGATCTCAGGCAATGCCAAGTTGAGGAGAGCT
GTGATGACCATTCTGCTCTGGGCTCAGAGCAGCCTGAAGGTAAGAGCCGACCACAAGGCA
GATTCCCGGACACTGTGCTGA (SEQ ID NO: 1)

hT2R51 Conceptual Translation (BAC AC011654) (SEQ ID NO: 173)

MLTLTRIRTVSYEVRSTFLFISVLEFAVGFLTNAFVFLVNFWDVVKRQALSNSDCVLLCLSISRL
FLHGLLFLSAIQLTHFQKLSEPLNHSYQAIIMLWMIANQANLWLAACLSLLYCSKLIRFSHTFLI
CLASWVSRKISQMLLGIILCSCICTVLCVWCFFSRPHFTVTTVLFMNNNTRLNWQIKDLNLFYS
FLFCYLWSVPPFLLFLVSSGMLTVSLGRHMRTMKVYTRNSRDPSLEAHIKALKSLVSFFCFFVIS
SCVAFISVPLLILWRDKIGVMVCVGIMAACPSGHAAILISGNAKLRRAVMTILLWAQSSLKVRA
DHKADSRTLC (SEQ ID NO: 2)

hT2R54 Full-Length cDNA (BAC AC024156) (SEQ ID NO: 174)

ATGACTAAACTCTGCGATCCTGCAGAAAGTGAATTGTCGCCATTTCTCATCACCTTAATTTT
AGCAGTTTTACTTGCTGAATACCTCATTGGTATCATTGCAAATGGTTTCATCATGGCTATAC
ATGCAGCTGAATGGGTTCAAAATAAGGCAGTTTCCACAAGTGGCAGGATCCTGGTTTTCCT
GAGTGTATCCAGAATAGCTCTCCAAAGCCTCATGATGTTAGAAATTACCATCAGCTCAACC
TCCCTAAGTTTTTATTCTGAAGACGCTGTATATTATGCATTCAAAATAAGTTTTATATTCTT
AAATTTTTGTAGCCTGTGGTTTGCTGCCTGGCTCAGTTTCTTCTACTTTGTGAAGATTGCCA
ATTTCTCCTACCCCCTTTTCCTCAAACTGAGGTGGAGAATTACTGGATTGATACCCTGGCTT
CTGTGGCTGTCCGTGTTTATTTCCTTCAGTCACAGCATGTTCTGCATCAACATCTGCACTGT
GTATTGTAACAATTCTTTCCCTATCCACTCCTCCAACTCCACTAAGAAAACATACTTGTCTG
AGATCAATGTGGTCGGTCTGGCTTTTTTCTTTAACCTGGGGATTGTGACTCCTCTGATCATG
TTCATCCTGACAGCCACCCTGCTGATCCTCTCTCTCAAGAGACACACCCTACACATGGGAA
GCAATGCCACAGGGTCCAACGACCCCAGCATGGAGGCTCACATGGGGGCCATCAAAGCTA
TCAGCTACTTTCTCATTCTCTACATTTTCAATGCAGTTGCTCTGTTTATCTACCTGTCCAAC
ATGTTTGACATCAACAGTCTGTGGAATAATTTGTGCCAGATCATCATGGCTGCCTACCCTG
CCAGCCACTCAATTCTACTGATTCAAGATAACCCTGGGCTGAGAAGAGCCTGGAAGCGGCT
TCAGCTTCGACTTCATCTTTACCCAAAAGAGTGGACTCTGTGA (SEQ ID NO: 3)

hT2R54 Conceptual Translation (BAC AC024156) (SEQ ID NO: 175)

MTKLCDPAESELSPFLITLILAVLLAEYLIGIIANGFIMAIHAAEWVQNKAVSTSGRILVFLSVSRI
ALQSLMMLEITISSTSLSFYSEDAVYYAFKISFIFLNFCSLWFAAWLSFFYFVKIANFSYPLFLKL
RWRITGLIPWLLWLSVFISFSHSMFCINICTVYCNNSFPIHSSNSTKKTYLSEINVVGLAFFFNLGI
VTPLIMFILTATLLILSLKRHTLHMGSNATGSNDPSMEAHMGAIKAISYFLILYIFNAVALFIYLS
NMFDINSLWNNLCQIIMAAYPASHSILLIQDNPGLRRAWKRLQLRLHLYPKEWTL (SEQ ID
NO: 4)

hT2R55 Full-Length cDNA (BAC AC024156) (SEQ ID NO: 176)

ATGGCAACGGTGAACACAGATGCCACAGATAAAGACATATCCAAGTTCAAGGTCACCTTC
ACTTTGGTGGTCTCCGGAATAGAGTGCATCACTGGCATCCTTGGGAGTGGCTTCATCACGG
CCATCTATGGGGCTGAGTGGGCCAGGGGCAAAACACTCCCCACTGGTGACCGCATTATGTT
GATGCTGAGCTTTTCCAGGCTCTTGCTACAGATTTGGATGATGCTGGAGAACATTTTCAGT
CTGCTATTCCGAATTGTTTATAACCAAAACTCAGTGTATATCCTCTTCAAAGTCATCACTGT
CTTTCTGAACCATTCCAATCTCTGGTTTGCTGCCTGGCTCAAAGTCTTCTATTGTCTTAGAA
TTGCAAACTTCAATCATCCTTTGTTCTTCCTGATGAAGAGGAAAATCATAGTGCTGATGCC

TTGGCTTCTCAGGCTGTCAGTGTTGGTTTCCTTAAGCTTCAGCTTTCCTCTCTCGAGAGATG
TCTTCAATGTGTATGTGAATAGCTCCATTCCTATCCCCTCCTCCAACTCCACGGAGAAGAA
GTACTTCTCTGAGACCAATATGGTCAACCTGGTATTTTTCTATAACATGGGGATCTTCGTTC
CTCTGATCATGTTCATCCTGGCAGCCACCCTGCTGATCCTCTCTCTCAAGAGACACACCCTA
CACATGGGAAGCAATGCCACAGGGTCCAGGGACCCCAGCATGAAGGCTCACATAGGGGCC
ATCAAAGCCACCAGCTACTTTCTCATCCTCTACATTTTCAATGCAATTGCTCTATTTCTTTC
CACGTCCAACATCTTTGACACTTACAGTTCCTGGAATATTTTGTGCAAGATCATCATGGCT
GCCTACCCTGCCGGCCACTCAGTACAACTGATCTTGGGCAACCCTGGGCTGAGAAGAGCCT
GGAAGCGGTTTCAGCACCAAGTTCCTCTTTACCTAAAAGGGCAGACTCTGTGA (SEQ ID
NO: 5)

hT2R55 Conceptual Translation (BAC AC024156) (SEQ ID NO: 177)

MATVNTDATDKDISKFKVTFTLVVSGIECITGILGSGFITAIYGAEWARGKTLPTGDRIMLMLSF
SRLLLQIWMMLENIFSLLFRIVYNQNSVYILFKVITVFLNHSNLWFAAWLKVFYCLRIANFNHP
LFFLMKRKIIVLMPWLLRLSVLVSLSFSFPLSRDVFNVYVNSSIPIPSSNSTEKKYFSETNMVNLV
FFYNMGIFVPLIMFILAATLLILSLKRHTLHMGSNATGSRDPSMKAHIGAIKATSYFLILYIFNAI
ALFLSTSNIFDTYSSWNILCKIIMAAYPAGHSVQLILGNPGLRRAWKRFQHQVPLYLKGQTL
(SEQ ID NO: 6)

hT2R61 Full-Length cDNA (BAC AC018630) (SEQ ID NO: 178)

ATGATAACTTTTCTACCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGAAA
TTTTGCTAATGGCTTCATAGCACTGGTAAATTCCATTGAGTGGTTCAAGAGACAAAAGATC
TCCTTTGCTGACCAAATTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTTGCTCTGGGTATT
ATTATTAAACTGGTATTCAACTGTGTTGAATCCAGCTTTTAATAGTGTAGAAGTAAGAACT
ACTGCTTATAATATCTGGGCAGTGATCAACCATTTCAGCAACTGGCTTGCTACTACCCTCA
GCATATTTTATTTGCTCAAGATTGCCAATTTCTCCAACTTTATTTTTCTTCACTTAAAGAGG
AGAGTTAAGAGTGTCATTCTGGTGATGTTGTTGGGGCCTTTGCTATTTTTGGCTTGTCATCT
TTTTGTGATAAACATGAATGAGATTGTGCGGACAAAAGAATTTGAAGGAAACATGACTTG
GAAGATCAAATTGAAGAGTGCAATGTACTTTTCAAATATGACTGTAACCATGGTAGCAAA
CTTAGTACCCTTCACTCTGACCCTACTATCTTTTATGCTGTTAATCTGTTCTTTGTGTAAAC
ATCTCAAGAAGATGCAGCTCCATGGTAAAGGATCTCAAGATCCCAGCACCAAGGTCCACA
TAAAAGCTTTGCAAACTGTGATCTCCTTCCTCTTGTTATGTGCCATTTACTTTCTGTCCATA
ATGATATCAGTTTGGAGTTTTGGAAGTCTGGAAAACAAACCTGTCTTCATGTTCTGCAAAG
CTATTAGATTCAGCTATCCTTCAATCCACCCATTCATCCTGATTTGGGGAAACAAGAAGCT
AAAGCAGACTTTTCTTTCAGTTTTTTGGCAAATGAGGTACTGGGTGAAAGGAGAGAAGACT
TCATCTCCATAG (SEQ ID NO: 7)

hT2R61 Conceptual Translation (BAC AC018630) (SEQ ID NO: 179)

MITFLPIIFSSLVVVTFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLWVLLLNW
YSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATTLSIFYLLKIANFSNFIFLHLKRRVKSVILV
MLLGPLLFLACHLFVINMNEIVRTKEFEGNMTWKIKLKSAMYFSNMTVTMVANLVPFTLTLLS
FMLLICSLCKHLKKMQLHGKGSQDPSTKVHIKALQTVISFLLLCAIYFLSIMISVWSFGSLENKP
VFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFWQMRYWVKGEKTSSP (SEQ ID NO: 8)

hT2R63 Full-Length cDNA (BAC AC018630) (SEQ ID NO: 180)

ATGATGAGTTTTCTACACATTGTTTTTTCCATTCTAGTAGTGGTTGCATTTATTCTTGGAAA
TTTTGCCAATGGCTTTATAGCACTGATAAATTTCATTGCCTGGGTCAAGAGACAAAAGATC
TCCTCAGCTGATCAAATTATTGCTGCTCTGGCAGTCTCCAGAGTTGGTTTGCTCTGGGTAA
TATTATTACATTGGTATTCAACTGTGTTGAATCCAACTTCATCTAATTTAAAAGTAATAATT
TTTATTTCTAATGCCTGGGCAGTAACCAATCATTTCAGCATCTGGCTTGCTACTAGCCTCAG
CATATTTTATTTGCTCAAGATCGTCAATTTCTCCAGACTTATTTTTCATCACTTAAAAAGGA
AGGCTAAGAGTGTAGTTCTGGTGATAGTGTTGGGGTCTTTGTTCTTTTTGGTTTGTCACCTT
GTGATGAAACACACGTATATAAATGTGTGGACAGAAGAATGTGAAGGAAACGTAACTTGG

AAGATCAAACTGAGGAATGCAATGCACCTTTCCAACTTGACTGTAGCCATGCTAGCAAACT
TGATACCATTCACTCTGACCCTGATATCTTTTCTGCTGTTAATCTACTCTCTGTGTAAACAT
CTGAAGAAGATGCAGCTCCATGGCAAAGGATCTCAAGATCCCAGCACCAAGATCCACATA
AAAGCTCTGCAAACTGTGACCTCCTTCCTCATATTACTTGCCATTTACTTTCTGTGTCTAAT
CATATCGTTTTGGAATTTTAAGATGCGACCAAAAGAAATTGTCTTAATGCTTTGCCAAGCT
TTTGGAATCATATATCCATCATTCCACTCATTCATTCTGATTTGGGGGAACAAGACGCTAA
AGCAGACCTTTCTTTCAGTTTTGTGGCAGGTGACTTGCTGGGCAAAAGGACAGAACCAGTC
AACTCCATAG (SEQ ID NO. 9)

hT2R63 Conceptual Translation (BAC AC018630) (SEQ ID NO: 181)

MMSFLHIVFSILVVVAFILGNFANGFIALINFIAWVKRQKISSADQIIAALAVSRVGLLWVILLH
WYSTVLNPTSSNLKVIIFISNAWAVTNHFSIWLATSLSIFYLLKIVNFSRLIFHHLKRKAKSVVLV
IVLGSLFFLVCHLVMKHTYINVWTEECEGNVTWKIKLRNAMHLSNLTVAMLANLIPFTLTLISF
LLLIYSLCKHLKKMQLHGKGSQDPSTKIHIKALQTVTSFLILLAIYFLCLIISFWNFKMRPKEIVL
MLCQAFGIIYPSFHSFILIWGNKTLKQTFLSVLWQVTCWAKGQNQSTP (SEQ ID NO: 10)

hT2R64 Full-Length cDNA (BAC AC018630) (SEQ ID NO: 182)

ATGACAACTTTTATACCCATCATTTTTTCCAGTGTGGTAGTGGTTCTATTTGTTATTGGAAA
TTTTGCTAATGGCTTCATAGCATTGGTAAATTCCATTGAGCGGGTCAAGAGACAAAAGATC
TCTTTTGCTGACCAGATTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTTGCTCTGGGTATT
ATTATTAAATTGGTATTCAACTGTGTTTAATCCAGCTTTTTATAGTGTAGAAGTAAGAACT
ACTGCTTATAATGTCTGGGCAGTAACCGGCCATTTCAGCAACTGGCTTGCTACTAGCCTCA
GCATATTTTATTTGCTCAAGATTGCCAATTTCTCCAACCTTATTTTTCTTCACTTAAAGAGG
AGAGTTAAGAGTGTCATTCTGGTGATGCTGTTGGGGCCTTTACTATTTTTGGCTTGTCAAC
TTTTTGTGATAAACATGAAAGAGATTGTACGGACAAAAGAATATGAAGGAAACTTGACTT
GGAAGATCAAATTGAGGAGTGCAGTGTACCTTTCAGATGCGACTGTAACCACGCTAGGAA
ACTTAGTGCCCTTCACTCTGACCCTGCTATGTTTTTTGCTGTTAATCTGTTCTCTGTGTAAA
CATCTCAAGAAGATGCAGCTCCATGGTAAAGGATCTCAAGATCCCAGCACCAAGGTCCAC
ATAAAAGCTTTGCAAACTGTGATCTTTTTCCTCTTGTTATGTGCCGTTTACTTTCTGTCCAT
AATGATATCAGTTTGGAGTTTTGGGAGTCTGGAAAACAAACCTGTCTTCATGTTCTGCAAA
GCTATTAGATTCAGCTATCCTTCAATCCACCCATTCATCCTGATTTGGGGAAACAAGAAGC
TAAAGCAGACTTTTCTTTCAGTTTTGCGGCAAGTGAGGTACTGGGTGAAAGGAGAGAAGC
CTTCATCTCCATAG (SEQ ID NO: 11)

hT2R64 Conceptual Translation (BAC AC018630) (SEQ ID NO: 183)

MTTFIPIIFSSVVVVLFVIGNFANGFIALVNSIERVKRQKISFADQILTALAVSRVGLLWVLLLNW
YSTVFNPAFYSVEVRTTAYNVWAVTGHFSNWLATSLSIFYLLKIANFSNLIFLHLKRRVKSVIL
VMLLGPLLFLACQLFVINMKEIVRTKEYEGNLTWKIKLRSAVYLSDATVTTLGNLVPFTLTLLC
FLLLICSLCKHLKKMQLHGKGSQDPSTKVHIKALQTVIFFLLLCAVYFLSIMISVWSFGSLENKP
VFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVLRQVRYWVKGEKPSSP (SEQ ID NO: 12)

hT2R65 Full-Length cDNA (BAC AC018630) (SEQ ID NO: 184)

ATGATGTGTTTTCTGCTCATCATTTCATCAATTCTGGTAGTGTTTGCATTTGTTCTTGGAAA
TGTTGCCAATGGCTTCATAGCCCTAGTAAATGTCATTGACTGGGTTAACACACGAAAGATC
TCCTCAGCTGAGCAAATTCTCACTGCTCTGGTGGTCTCCAGAATTGGTTTACTCTGGGTCAT
GTTATTCCTTTGGTATGCAACTGTGTTTAATTCTGCTTTATATGGTTTAGAAGTAAGAATTG
TTGCTTCTAATGCCTGGGCTGTAACGAACCATTTCAGCATGTGGCTTGCTGCTAGCCTCAG
CATATTTTGTTTGCTCAAGATTGCCAATTTCTCCAACCTTATTTCTCTCCACCTAAAGAAGA
GAATTAAGAGTGTTGTTCTGGTGATACTGTTGGGGCCCTTGGTATTTCTGATTTGTAATCTT
GCTGTGATAACCATGGATGAGAGAGTGTGGACAAAAGAATATGAAGGAAATGTGACTTGG
AAGATCAAATTGAGGAATGCAATACACCTTTCAAGCTTGACTGTAACTACTCTAGCAAACC
TCATACCCTTTACTCTGAGCCTAATATGTTTTCTGCTGTTAATCTGTTCTCTTTGTAAACAT
CTCAAGAAGATGCGGCTCCATAGCAAAGGATCTCAAGATCCCAGCACCAAGGTCCATATA

AAAGCTTTGCAAACTGTGACCTCCTTCCTCATGTTATTTGCCATTTACTTTCTGTGTATAAT
CACATCAACTTGGAATCTTAGGACACAGCAGAGCAAACTTGTACTCCTGCTTTGCCAAACT
GTTGCAATCATGTATCCTTCATTCCACTCATTCATCCTGATTATGGGAAGTAGGAAGCTAA
AACAGACCTTTCTTTCAGTTTTGTGGCAGATGACACGCTGA (SEQ ID NO: 13)

hT2R65 Conceptual Translation (BAC AC018630) (SEQ ID NO: 185)

MMCFLLIISSILVVFAFVLGNVANGFIALVNVIDWVNTRKISSAEQILTALVVSRIGLLWVMLFL
WYATVFNSALYGLEVRIVASNAWAVTNHFSMWLAASLSIFCLLKIANFSNLISLHLKKRIKSVV
LVILLGPLVFLICNLAVITMDERVWTKEYEGNVTWKIKLRNAIHLSSLTVTTLANLIPFTLSLICF
LLLICSLCKHLKKMRLHSKGSQDPSTKVHIKALQTVTSFLMLFAIYFLCIITSTWNLRTQQSKLV
LLLCQTVAIMYPSFHSFILIMGSRKLKQTFLSVLWQMTR (SEQ ID NO: 14)

hT2R67 Full-Length cDNA (BAC AC018630) (SEQ ID NO: 186)

ATGATAACTTTTCTATACATTTTTTTTTCAATTCTAATAATGGTTTTATTTGTTCTCGGAAA
CTTTGCCAATGGCTTCATAGCACTGGTAAATTTCATTGACTGGGTGAAGAGAAAAAAGATC
TCCTCAGCTGACCAAATTCTCACTGCTCTGGCGGTCTCCAGAATTGGTTTGCTCTGGGCATT
ATTATTAAATTGGTATTTAACTGTGTTGAATCCAGCTTTTTATAGTGTAGAATTAAGAATT
ACTTCTTATAATGCCTGGGTTGTAACCAACCATTTCAGCATGTGGCTTGCTGCTAACCTCA
GCATATTTTATTTGCTCAAGATTGCCAATTTCTCCAACCTTCTTTTTCTTCATTTAAAGAGG
AGAGTTAGGAGTGTCATTCTGGTGATACTGTTGGGGACTTTGATATTTTTGGTTTGTCATC
TTCTTGTGGCAAACATGGATGAGAGTATGTGGGCAGAAGAATATGAAGGAAACATGACTG
GGAAGATGAAATTGAGGAATACAGTACATCTTTCATATTTGACTGTAACTACCCTATGGAG
CTTCATACCCTTTACTCTGTCCCTGATATCTTTTCTGATGCTAATCTGTTCTCTGTGTAAAC
ATCTCAAGAAGATGCAGCTCCATGGAGAAGGATCGCAAGATCTCAGCACCAAGGTCCACA
TAAAAGCTTTGCAAACTCTGATCTCCTTCCTCTTGTTATGTGCCATTTTCTTTCTATTCCTA
ATCGTTTCGGTTTGGAGTCCTAGGAGGCTGCGGAATGACCCGGTTGTCATGGTTAGCAAGG
CTGTTGGAAACATATATCTTGCATTCGACTCATTCATCCTAATTTGGAGAACCAAGAAGCT
AAAACACACCTTTCTTTTGATTTTGTGTCAGATTAGGTGCTGA (SEQ ID NO: 15)

hT2R67 Conceptual Translation (BAC AC018630) (SEQ ID NO: 187)

MITFLYIFFSILIMVLFVLGNFANGFIALVNFIDWVKRKKISSADQILTALAVSRIGLLWALLLNW
YLTVLNPAFYSVELRITSYNAWVVTNHFSMWLAANLSIFYLLKIANFSNLLFLHLKRRVRSVIL
VILLGTLIFLVCHLLVANMDESMWAEEYEGNMTGKMKLRNTVHLSYLTVTTLWSFIPFTLSLIS
FLMLICSLCKHLKKMQLHGEGSQDLSTKVHIKALQTLISFLLLCAIFFLFLIVSVWSPRRLRNDP
VVMVSKAVGNIYLAFDSFILIWRTKKLKHTFLLILCQIRC (SEQ ID NO: 16)

hT2R71 Full-Length cDNA (BAC AC073264) (SEQ ID NO: 188)

ATGCAAGCAGCACTGACGGCCTTCTTCGTGTTGCTCTTTAGCCTGCTGAGTCTTCTGGGGA
TTGCAGCGAATGGCTTCATTGTGCTGGTGCTGGGCAGGGAGTGGCTGCGATATGGCAGGT
TGCTGCCCTTGGATATGATCCTCATTAGCTTGGGTGCCTCCCGCTTCTGCCTGCAGTTGGTT
GGGACGGTGCACAACTTCTACTACTCTGCCCAGAAGGTCGAGTACTCTGGGGGTCTCGGCC
GACAGTTCTTCCATCTACACTGGCACTTCCTGAACTCAGCCACCTTCTGGTTTTGCAGCTGG
CTCAGTGTCCTGTTCTGTGTGAAGATTGCTAACATCACACACTCCACCTTCCTGTGGCTGA
AGTGGAGGTTCCCAGGGTGGGTGCCCTGGCTCCTGTTGGGCTCTGTCCTGATCTCCTTCAT
CATAACCCTGCTGTTTTTTTGGGTGAACTACCCTGTATATCAAGAATTTTTAATTAGAAAAT
TTTCTGGGAACATGACCTACAAGTGGAATACAAGGATAGAAACATACTATTTCCCATCCCT
GAAACTGGTCATCTGGTCAATTCCTTTTTCTGTTTTTCTGGTCTCAATTATGCTGTTAATTA
ATTCTCTGAGGAGGCATACTCAGAGAATGCAGCACAACGGGCACAGCCTGCAGGACCCCA
GCACCCAGGCTCACACCAGAGCTCTGAAGTCCCTCATCTCCTTCCTCATTCTTTATGCTCTG
TCCTTTCTGTCCCTGATCATTGATGCCGCAAAATTTATCTCCATGCAGAACGACTTTTACTG
GCCATGGCAAATTGCAGTCTACCTGTGCATATCTGTCCATCCCTTCATCCTCATCTTCAGCA
ACCTCAAGCTTCGAAGCGTGTTCTCGCAGCTCCTGTTGTTGGCAAGGGGCTTCTGGGTGGC
CTAG (SEQ ID NO: 17)

hT2R71 Conceptual Translation (BAC AC073264) (SEQ ID NO: 189)

MQAALTAFFVLLFSLLSLLGIAANGFIVLVLGREWLRYGRLLPLDMILISLGASRFCLQLVGTVH
NFYYSAQKVEYSGGLGRQFFHLHWHFLNSATFWFCSWLSVLFCVKIANITHSTFLWLKWRFPG
WVPWLLLGSVLISFIITLLFFWVNYPVYQEFLIRKFSGNMTYKWNTRIETYYFPSLKLVIWSIPFS
VFLVSIMLLINSLRRHTQRMQHNGHSLQDPSTQAHTRALKSLISFLILYALSFLSLIIDAAKFISM
QNDFYWPWQIAVYLCISVHPFILIFSNLKLRSVFSQLLLLARGFWVA (SEQ ID NO: 18)

hT2R75 Full-Length cDNA (SEQ ID NO: 190)

ATGATAACTTTTCTGCCCATCATTTTTTCCATTCTAATAGTGGTTACATTTGTGATTGGAAA
TTTTGCTAATGGCTTCATAGCATTGGTAAATTCCATTGAGTGGTTCAAGAGACAAAAGATC
TCTTTTGCTGACCAAATTCTCACTGCTCTGGCAGTCTCCAGAGTTGGTTTACTCTGGGTATT
AGTATTAAATTGGTATGCAACTGAGTTGAATCCAGCTTTTAACAGTATAGAAGTAAGAATT
ACTGCTTACAATGTCTGGGCAGTAATCAACCATTTCAGCAACTGGCTTGCTACTAGCCTCA
GCATATTTTATTTGCTCAAGATTGCCAATTTCTCCAACCTTATTTTTCTTCACTTAAAGAGG
AGAGTTAAGAGTGTTGTTCTGGTGATACTATTGGGGCCTTTGCTATTTTTGGTTTGTCATCT
TTTTGTGATAAACATGAATCAGATTATATGGACAAAAGAATATGAAGGAAACATGACTTG
GAAGATCAAACTGAGGAGTGCAATGTACCTTTCAAATACAACGGTAACCATCCTAGCAAA
CTTAGTTCCCTTCACTCTGACCCTGATATCTTTTCTGCTGTTAATCTGTTCTCTGTGTAAAC
ATCTCAAAAAGATGCAGCTCCATGGCAAAGGATCTCAAGATCCCAGCATGAAGGTCCACA
TAAAAGCTTTGCAAACTGTGACCTCCTTCCTCTTGTTATGTGCCATTTACTTTCTGTCCATA
ATCATGTCAGTTTGGAGTTTTGAGAGTCTGGAAAACAAACCTGTCTTCATGTTCTGCGAAG
CTATTGCATTCAGCTATCCTTCAACCCACCCATTCATCCTGATTTGGGGAAACAAGAAGCT
AAAGCAGACTTTTCTTTCAGTTTTGTGGCATGTGAGGTACTGGGTGAAAGGAGAGAAGCCT
TCATCTTCATAG (SEQ ID NO: 19)

hT2R75 Conceptual Translation cDNA (SEQ ID NO: 191)

MITFLPIIFSILIVVTFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLWVLVLNW
YATELNPAFNSIEVRITAYNVWAVINHFSNWLATSLSIFYLLKIANFSNLIFLHLKRRVKSVVLVI
LLGPLLFLVCHLFVINMNQIIWTKEYEGNMTWKIKLRSAMYLSNTTVTILANLVPFTLTLISFLL
LICSLCKHLKKMQLHGKGSQDPSMKVHIKALQTVTSFLLLCAIYFLSIIMSVWSFESLENKPVF
MFCEAIAFSYPSTHPFILIWGNKKLKQTFLSVLWHVRYWVKGEKPSSS (SEQ ID NO: 20)

hT2R59 Pseudogene (BAC AC018630) (SEQ ID NO: 192)

ATGGTATATTTTCTGCTCATCATTTTATCAATTCTGGTAGTGTTTGCATTTGTTCTTGGAAA
TTTTTCCAATGGCTTCATAGCTCTAGTAAATGTCATTGACTGGGTTAAGACACGAAAGATC
TCCTCAGCTGACCAAATCCTCACTGCTCTGGTGGTCTCCAGAATTGGTTTACTCTGGGTCAT
ATTATTACATTGGTATGCAAATGTGTTTAATTCAGCTTTATATAGTTCAGAAGTAGGAGCT
GTTGCTTCTAATATCTCAGCAATAATCAACCATTTCAGCATCTGGCTTGCTGCTAGCCTCAG
CATATTTTATTTGCTCAAGATTGCCAATTTCTCCAACCTTATTTTTCTCCACCTAAAGAAGA
GAATTAGGAGTGTTGTTCTGGTGATACTGTTGGGTCCCTTGGTATTTTTGATTTGTAATCTT
GCTGTGATAACCATGGATGACAGTGTGTGGACAAAAGAATATGAAGGAAATGTGACTTGG
AAGATCAAATTGAGGAATGCAATACACCTTTCAAACTTGACTGTAAGCACACTAGCAAACC
TCATACCCTTCATTCTGACCCTAATATGTTTTCTGCTGTTAATCTGTTCTCTGCATAAACAT
CTCAAGAAGATGCAGCTCCATGGCAAAGGATCTCAAGATCTCAGCACCAAGGTCCACATA
AAAGCTTTGCAAACTGTGATCTCCTTCCTCATGTTATATGCCATTTACTTTCTGTATCTAAT
CACATTAACCTGGAATCTTTGAACACAGCAGAACAAACTTGTATTCCTGCTTTGCCAAACT
CTTGGAATCATGTATCCTTCATTCCACTCATTCTTCCTGATTATGGGAAGCAGGAAACTAA
AACAGACGTTTCTTTCAGTTTTATGTCAGGTCACATGCTTAGTGAAAGGACAGCAACCCTC
AACTCCATAG (SEQ ID NO: 21)

hT2R69 Pseudogene (BAC AC018630) (SEQ ID NO: 193)

ATGATATGTTTTCTGCTCATCATTTTATCAATTCTGGTAGTGTTTGCATTTGTTCTTGGAAA
TGTTGCCAATGGCTTCATAGCTCTAGTAGGTGTCCTTGAGTGGGTTAAGACACAAAAGATC
TCATCAGCTGACCAAATTTCTCACTGCTCTGGTGGTGTCCAGAGTTGGTTTACTCTGGGTC
ATATTATTACATTGGTATGCAACTGTGTTTAATTTGGCTTCACATAGATTAGAAGTAAGAA
TTTTTGGTTCTAATGTCTCAGCAATAACCAAGCATTTCAGCATCTGGGTGTTACTAGCCTCA
GCATATTTCATTTGCTCAAGACTGCCAATTTCTCCAACCTTATTTTTCTCCACCTAAAGAAA
AGGATTAAGAATGTTGGTTTGGTGATGCTGTTGGGGCCCTTGGTATTTTTCATTTGTAATC
TTGCTCTGATAACCACGGGTGAGAGTGTGTGGACAAAAGAATATGAAGGAAATTTGTCTT
GGATGATCAAATTGAGGAATGCAATACAGCTTTCAAACTTGACTGTAACCATGCCAGCAA
ACGTCACACCCTGCACTCTGACACTAATATCTTTTCTGCTGTTAATCTATTCTCCATGTAAA
CATGTCAAGAAGATGCAGCTCCATGGCAAAGGATCTCAACATCTCAGCACCAAGGTGCAC
ATAAAAGCTTTGCAAACTGTGATCTCCTTCCTTATGTTATTTGCCATTTACTTTCTGTGTCT
AATCACATCAACTTGGAATCCTAGGACTCAGCAGAGCAAACTTGTATTCCTGCTTTACCAA
ACTCTTGGATTCATGTATCTTTTGTTCCACTCATTCATCCTGACTATGGGAAGTAGGAAGCC
AAAACAGACCTTTCTTTCAGCTTTGTGA (SEQ ID NO: 22)

mT2R33 Full-Length cDNA (BAC AC020619) (SEQ ID NO: 194)

ATGACCTCCCCTTTCCCAGCTATTTATCACATGGTCATCATGACAGCAGAGTTTCTCATCGG
GACTACAGTGAATGGATTCCTTATCATTGTGAACTGCTATGACTTGTTCAAGAGCCGAACG
TTCCTGATCCTGCAGACCCTCTTGATGTGCACAGGGCTGTCCAGACTCGGTCTGCAGATAA
TGCTCATGACCCAAAGCTTCTTCTCTGTGTTCTTTCCATACTCTTATGAGGAAAATATTTAT
AGTTCAGATATAATGTTCGTCTGGATGTTCTTCAGCTCGATTGGCCTCTGGTTTGCCACATG
TCTCTCTGTCTTTTACTGCCTCAAGATTTCAGGCTTCACTCCACCCTGGTTTCTTTGGCTGA
AATTCAGAATTTCAAAGCTCATATTTTGGCTGCTTCTGGGCAGCTTGCTGGCCTCTCTGGG
CACTGCAACTGTGTGCATCGAGGTAGGTTTCCCTTTAATTGAGGATGGCTATGTCCTGAGA
AACGCAGGACTAAATGATAGTAATGCCAAGCTAGTGAGAAATAATGACTTGCTCCTCATC
AACCTGATCCTCCTGCTTCCCCTGTCTGTGTTTGTGATGTGCACCTCTATGTTATTTGTTTC
TCTTTACAAGCACATGCACTGGATGCAAAGCGAATCTCACAAGCTGTCAAGTGCCAGAACC
GAAGCTCATATAAATGCATTAAAGACAGTGACAACATTCTTTTGTTTCTTTGTTTCTTACTT
TGCTGCCTTCATGGCAAATATGACATTTAGAATTCCATACAGAAGTCATCAGTTCTTCGTG
GTGAAGGAAATCATGGCAGCATATCCCGCCGGCCACTCTGTCATAATCGTCTTGAGTAACT
CTAAGTTCAAAGACTTATTCAGGAGAATGATCTGTCTACAGAAGGAAGAGTGA (SEQ ID
NO: 23)

mT2R33 Conceptual Translation (BAC AC020619) (SEQ ID NO: 195)

MTSPFPAIYHMVIMTAEFLIGTTVNGFLIIVNCYDLFKSRTFLILQTLLMCTGLSRLGLQIMLMT
QSFFSVFFPYSYEENIYSSDIMFVWMFFSSIGLWFATCLSVFYCLKISGFTPPWFLWLKFRISKLIF
WLLLGSLLASLGTATVCIEVGFPLIEDGYVLRNAGLNDSNAKLVRNNDLLLINLILLLPLSVFVM
CTSMLFVSLYKHMHWMQSESHKLSSARTEAHINALKTVTTFFCFFVSYFAAFMANMTFRIPYR
SHQFFVVKEIMAAYPAGHSVIIVLSNSKFKDLFRRMICLQKEE (SEQ ID NO: 24)

SEQ. ID NO: 196

Amino Acid Sequence rT1R3

MPGLAILGLSLAAFLELGMGSSLCLSQQFKAQGDYILGGLFPLGTTEEATLNQRTQPNGI

LCTRFSPLGLFLAMAMKMAVEEINNGSALLPGLRLGYDLFDTCSEPVVTMKPSLMFMAKV

GSQSIAAYCNYTQYQPRVLAVIGPHSSELALITGKFFSFFLMPQVSYSASMDRLSDRETF
PSFFRTVPSDRVQLQAVVTLLQNFSWNWVAALGSDDDYGREGLSIFSGLANSRGICIAHE
GLVPQHDTSGQQLGKVVDVLRQVNQSKVQVVVLFASARAVYSLFSYSILHDLSPKVWVAS
ESWLTSDLVMTLPNIARVGTVLGFLQRGALLPEFSHYVETRLALAADPTFCASLKAELDL
EERVMGPRCSQCDYIMLQNLSSGLMQNLSAGQLHHQIFATYAAVYSVAQALHNTLQCNVS
HCHTSEPVQPWQLLENMYNMSFRARDLTLQFDAKGSVDMEYDLKMWVWQSPTPVLHTVGT
FNGTLQLQHSKMYWPGNQVPVSQCSRQCKDGQVRRVKGFHSCCYDCVDCKAGSYRKHPDD
FTCTPCGKDQWSPEKSTTCLPRRPKFLAWGEPAVLSLLLLLCLVLGLTLAALGLFVHYWD
SPLVQASGGSLFCFGLICLGLFCLSVLLFPGRPRSASCLAQQPMAHLPLTGCLSTLFLQA
AEIFVESELPLSWANWLCSYLRGPWAWLVVLLATLVEAALCAWYLMAFPPEVVTDWQVLP
TEVLEHCRMRSWVSLGLVHITNAVLAFLCFLGTFLVQSQPGRYNRARGLTFAMLAYFIIW
VSFVPLLANVQVAYQPAVQMGAILFCALGILATFHLPKCYVLLWLPELNTQEFFLGRSPK
EASDGNSGSSEATRGHSE

SEQ. ID NO: 197

Amino Acid Sequence hT1R1

MLLCTARLVGLQLLISCCWAFACHSTESSPDFTLPGDYLLAGLFPLHSGCLQVRHRPEVT
LCDRSCSFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLS
LPGQHHIELQGDLLHYSPTVLAVIGPDSTNRAATTAALLSPFLVPMISYAASSETLSVKR
QYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQATGQGICIA
FKDIMPFSAQVGDERMQCLMRHLAQAGATVVVVFSSRQLARVFFESVVLTNLTGKVWVAS
EAWALSRHITGVPGIQRIGMVLGVAIQKRAVPGLKAFEEAYARADKKAPRPCHKGSWCSS
NQLCRECQAFMAHTMPKLKAFSMSSAYNAYRAVYAVAHGLHQLLGCASGACSRGRVYPWQ
LLEQIHKVHFLLHKDTVAFNDNRDPLSSYNIIAWDWNGPKWTFTVLGSSTWSPVQLNINE
TKIQWHGKDNQVPKSVCSSDCLEGHQRVVTGFHHCCFECVPCGAGTFLNKSDLYRCQPCG
KEEWAPEGSQTCFPRTVVFLALREHTSWVLLAANTLLLLLLLGTAGLFAWHLDTPVVRSA
GGRLCFLMLGSLAAGSGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIF
KFSTKVPTFYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPHLVMLEC
TETNSLGFILAFLYNGLLSISAFACSYLGKDLPENYNEAKCVTFSLLFNFVSWIAFFTTA

SVYDGKYLPAANMMAGLSSLSSGFGGYFLPKCYVILCRPDLNSTEHFQASIQDYTRRCGS
T

SEQ. ID NO: 198

Amino Acid Sequence hT1R2

MGPRAKTICSLFFLLWVLAEPAENSDFYLPGDYLLGGLFSLHANMKGIVHLNFLQVPMCK
EYEVKVIGYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN
LLPIQEDYSNYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELRDKVRFPAL
LRTTPSADHHVEAMVQLMLHFRWNWIIVLVSSDTYGRDNGQLLGERVARRDICIAFQETL
PTLQPNQNMTSEERQRLVTIVDKLQQSTARVVVVFSPDLTLYHFFNEVLRQNFTGAVWIA
SESWAIDPVLHNLTELGHLGTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCN
QECDNCLNATLSFNTILRLSGERVVYSVYSAVYAVAHALHSLLGCDKSTCTKRVVYPWQL
LEEIWKVNFTLLDHQIFFDPQGDVALHLEIVQWQWDRSQNPFQSVASYYPLQRQLKNIQD
ISWHTVNNTIPMSMCSKRCQSGQKKKPVGIHVCCFECIDCLPGTFLNHTEDEYECQACPN
NEWSYQSETSCFKRQLVFLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG
GPMCFLMLTLLLVAYMVVPVYVGPPKVSTCLCRQALFPLCFTICISCIAVRSFQIVCAFK
MASRFPRAYSYWVRYQGPYVSMAFITVLKMVIVVIGMLATGLSPTTRTDPDDPKITIVSC
NPNYRNSLLFNTSLDLLLSVVGFSFAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM
SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRRD

SEQ. ID NO: 199

Amino Acid Sequence hT1R3

MLGPAVLGLSLWALLHPGTGAPLCLSQQLRMKGDYVLGGLFPLGEAEEAGLRSRTRPSSP
VCTRFSSNGLLWALAMKMAVEEINNKSDLLPGLRLGYDLFDTCSEPVVAMKPSLMFLAKA
GSRDIAAYCNYTQYQPRVLAVIGPHSSELAMVTGKFFSFFLMPQVSYGASMELLSARETF
PSFFRTVPSDRVQLTAAAELLQEFGWNWVAALGSDDEYGRQGLSIFSALAAARGICIAHE
GLVPLPRADDSRLGKVQDVLHQVNQSSVQVVLLFASVHAAHALFNYSISSRLSPKVWVAS
EAWLTSDLVMGLPGMAQMGTVLGFLQRGAQLHEFPQYVKTHLALATDPAFCSALGEREQG
LEEDVVGQRCPQCDCITLQNVSAGLNHHQTFSVYAAVYSVAQALHNTLQCNASGCPAQDP
VKPWQLLENMYNLTFHVGGLPLRFDSSGNVDMEYDLKLWVWQGSVPRLHDVGRFNGSLRT

ERLKIRWHTSDNQKPVSRCSRQCQEGQVRRVKGFHSCCYDCVDCEAGSYRQNPDDIACTF
CGQDEWSPERSTRCFRRRSRFLAWGEPAVLLLLLLLSLALGLVLAALGLFVHHRDSPLVQ
ASGGPLACFGLVCLGLVCLSVLLFPGQPSPARCLAQQPLSHLPLTGCLSTLFLQAAEIFV
ESELPLSWADRLSGCLRGPWAWLVVLLAMLVEVALCTWYLVAFPPEVVTDWHMLPTEALV
HCRTRSWVSFGLAHATNATLAFLCFLGTFLVRSQPGRYNRARGLTFAMLAYFITWVSFVP
LLANVQVVLRPAVQMGALLLCVLGILAAFHLPRCYLLMRQPGLNTPEFFLGGGPGDAQGQ
NDGNTGNQGKHE

SEQ. ID NO: 200

Nucleic Acid Sequence hT1R1

ATGCTGCTCTGCACGGCTCGCCTGGTCGGCCTGCAGCTTCTCATTTCCTGCTGCTGGGCC
TTTGCCTGCCATAGCACGGAGTCTTCTCCTGACTTCACCCTCCCCGGAGATTACCTCCTG
GCAGGCCTGTTCCCTCTCCATTCTGGCTGTCTGCAGGTGAGGCACAGACCCGAGGTGACC
CTGTGTGACAGGTCTTGTAGCTTCAATGAGCATGGCTACCACCTCTTCCAGGCTATGCGG
CTTGGGGTTGAGGAGATAAACAACTCCACGGCCCTGCTGCCCAACATCACCCTGGGGTAC
CAGCTGTATGATGTGTGTTCTGACTCTGCCAATGTGTATGCCACGCTGAGAGTGCTCTCC
CTGCCAGGGCAACACCACATAGAGCTCCAAGGAGACCTTCTCCACTATTCCCCTACGGTG
CTGGCAGTGATTGGGCCTGACAGCACCAACCGTGCTGCCACCACAGCCGCCCTGCTGAGC
CCTTTCCTGGTGCCCATGATTAGCTATGCGGCCAGCAGCGAGACGCTCAGCGTGAAGCGG
CAGTATCCCTCTTTCCTGCGCACCATCCCCAATGACAAGTACCAGGTGGAGACCATGGTG
CTGCTGCTGCAGAAGTTCGGGTGGACCTGGATCTCTCTGGTTGGCAGCAGTGACGACTAT
GGGCAGCTAGGGGTGCAGGCACTGGAGAACCAGGCCACTGGTCAGGGGATCTGCATTGCT
TTCAAGGACATCATGCCCTTCTCTGCCCAGGTGGGCGATGAGAGGATGCAGTGCCTCATG
CGCCACCTGGCCCAGGCCGGGGCCACCGTCGTGGTTGTTTTTTCCAGCCGGCAGTTGGCC
AGGGTGTTTTTCGAGTCCGTGGTGCTGACCAACCTGACTGGCAAGGTGTGGGTCGCCTCA
GAAGCCTGGGCCCTCTCCAGGCACATCACTGGGGTGCCCGGGATCCAGCGCATTGGGATG
GTGCTGGGCGTGGCCATCCAGAAGAGGGCTGTCCCTGGCCTGAAGGCGTTTGAAGAAGCC
TATGCCCGGGCAGACAAGAAGGCCCCTAGGCCTTGCCACAAGGGCTCCTGGTGCAGCAGC
AATCAGCTCTGCAGAGAATGCCAAGCTTTCATGGCACACACGATGCCCAAGCTCAAAGCC
TTCTCCATGAGTTCTGCCTACAACGCATACCGGGCTGTGTATGCGGTGGCCCATGGCCTC

CACCAGCTCCTGGGCTGTGCCTCTGGAGCTTGTTCCAGGGGCCGAGTCTACCCCTGGCAG
CTTTTGGAGCAGATCCACAAGGTGCATTTCCTTCTACACAAGGACACTGTGGCGTTTAAT
GACAACAGAGATCCCCTCAGTAGCTATAACATAATTGCCTGGGACTGGAATGGACCCAAG
TGGACCTTCACGGTCCTCGGTTCCTCCACATGGTCTCCAGTTCAGCTAAACATAAATGAG
ACCAAAATCCAGTGGCACGGAAAGGACAACCAGGTGCCTAAGTCTGTGTGTTCCAGCGAC
TGTCTTGAAGGGCACCAGCGAGTGGTTACGGGTTTCCATCACTGCTGCTTTGAGTGTGTG
CCCTGTGGGGCTGGGACCTTCCTCAACAAGAGTGACCTCTACAGATGCCAGCCTTGTGGG
AAAGAAGAGTGGGCACCTGAGGGAAGCCAGACCTGCTTCCCGCGCACTGTGGTGTTTTTG
GCTTTGCGTGAGCACACCTCTTGGGTGCTGCTGGCAGCTAACACGCTGCTGCTGCTGCTG
CTGCTTGGGACTGCTGGCCTGTTTGCCTGGCACCTAGACACCCCTGTGGTGAGGTCAGCA
GGGGGCCGCCTGTGCTTTCTTATGCTGGGCTCCCTGGCAGCAGGTAGTGGCAGCCTCTAT
GGCTTCTTTGGGGAACCCACAAGGCCTGCGTGCTTGCTACGCCAGGCCCTCTTTGCCCTT
GGTTTCACCATCTTCCTGTCCTGCCTGACAGTTCGCTCATTCCAACTAATCATCATCTTC
AAGTTTTCCACCAAGGTACCTACATTCTACCACGCCTGGGTCCAAAACCACGGTGCTGGC
CTGTTTGTGATGATCAGCTCAGCGGCCCAGCTGCTTATCTGTCTAACTTGGCTGGTGGTG
TGGACCCCACTGCCTGCTAGGGAATACCAGCGCTTCCCCCATCTGGTGATGCTTGAGTGC
ACAGAGACCAACTCCCTGGGCTTCATACTGGCCTTCCTCTACAATGGCCTCCTCTCCATC
AGTGCCTTTGCCTGCAGCTACCTGGGTAAGGACTTGCCAGAGAACTACAACGAGGCCAAA
TGTGTCACCTTCAGCCTGCTCTTCAACTTCGTGTCCTGGATCGCCTTCTTCACCACGGCC
AGCGTCTACGACGGCAAGTACCTGCCTGCGGCCAACATGATGGCTGGGCTGAGCAGCCTG
AGCAGCGGCTTCGGTGGGTATTTTCTGCCTAAGTGCTACGTGATCCTCTGCCGCCCAGAC
CTCAACAGCACAGAGCACTTCCAGGCCTCCATTCAGGACTACACGAGGCGCTGCGGCTCC
ACCTGA

SEQ. ID NO: 201

Nucleic Acid Sequence hT1R3

ATGCTGGGCCCTGCTGTCCTGGGCCTCAGCCTCTGGGCTCTCCTGCACCCTGGGACGGGG
GCCCCATTGTGCCTGTCACAGCAACTTAGGATGAAGGGGGACTACGTGCTGGGGGGGCTG
TTCCCCCTGGGCGAGGCCGAGGAGGCTGGCCTCCGCAGCCGGACACGGCCCAGCAGCCCT
GTGTGCACCAGGTTCTCCTCAAACGGCCTGCTCTGGGCACTGGCCATGAAAATGGCCGTG

GAGGAGATCAACAACAAGTCGGATCTGCTGCCCGGGCTGCGCCTGGGCTACGACCTCTTT
GATACGTGCTCGGAGCCTGTGGTGGCCATGAAGCCCAGCCTCATGTTCCTGGCCAAGGCA
GGCAGCCGCGACATCGCCGCCTACTGCAACTACACGCAGTACCAGCCCCGTGTGCTGGCT
GTCATCGGGCCCCACTCGTCAGAGCTCGCCATGGTCACCGGCAAGTTCTTCAGCTTCTTC
CTCATGCCCCAggtcagCTACGGTGCTAGCATGGAGCTGCTGAGCGCCCGGGAGACCTTC
CCCTCCTTCTTCCGCACCGTGCCCAGCGACCGTGTGCAGCTGACGGCCGCCGCGGAGCTG
CTGCAGGAGTTCGGCTGGAACTGGGTGGCCGCCCTGGGCAGCGACGACGAGTACGGCCGG
CAGGGCCTGAGCATCTTCTCGGCCCTGGCCGCGGCACGCGGCATCTGCATCGCGCACGAG
GGCCTGGTGCCGCTGCCCCGTGCCGATGACTCGCGGCTGGGGAAGGTGCAGGACGTCCTG
CACCAGGTGAACCAGAGCAGCGTGCAGGTGGTGCTGCTGTTCGCCTCCGTGCACGCCGCC
CACGCCCTCTTCAACTACAGCATCAGCAGCAGGCTCTCGCCCAAGGTGTGGGTGGCCAGC
GAGGCCTGGCTGACCTCTGACCTGGTCATGGGGCTGCCCGGCATGGCCCAGATGGGCACG
GTGCTTGGCTTCCTCCAGAGGGGTGCCCAGCTGCACGAGTTCCCCCAGTACGTGAAGACG
CACCTGGCCCTGGCCACCGACCCGGCCTTCTGCTCTGCCCTGGGCGAGAGGGAGCAGGGT
CTGGAGGAGGACGTGGTGGGCCAGCGCTGCCCGCAGTGTGACTGCATCACGCTGCAGAAC
GTGAGCGCAGGGCTAAATCACCACCAGACGTTCTCTGTCTACGCAGCTGTGTATAGCGTG
GCCCAGGCCCTGCACAACACTCTTCAGTGCAACGCCTCAGGCTGCCCCGCGCAGGACCCC
GTGAAGCCCTGGCAGCTCCTGGAGAACATGTACAACCTGACCTTCCACGTGGGCGGGCTG
CCGCTGCGGTTCGACAGCAGCGGAAACGTGGACATGGAGTACGACCTGAAGCTGTGGGTG
TGGCAGGGCTCAGTGCCCAGGCTCCACGACGTGGGCAGGTTCAACGGCAGCCTCAGGACA
GAGCGCCTGAAGATCCGCTGGCACACGTCTGACAACCAGAAGCCCGTGTCCCGGTGCTCG
CGGCAGTGCCAGGAGGGCCAGGTGCGCCGGGTCAAGGGGTTCCACTCCTGCTGCTACGAC
TGTGTGGACTGCGAGGCGGGCAGCTACCGGCAAAACCCAGACGACATCGCCTGCACCTTT
TGTGGCCAGGATGAGTGGTCCCCGGAGCGAAGCACACGCTGCTTCCGCCGCAGGTCTCGG
TTCCTGGCATGGGGCGAGCCGGCTGTGCTGCTGCTGCTCCTGCTGCTGAGCCTGGCGCTG
GGCCTTGTGCTGGCTGCTTTGGGGCTGTTCGTTCACCATCGGGACAGCCCACTGGTTCAG
GCCTCGGGGGGGCCCCTGGCCTGCTTTGGCCTGGTGTGCCTGGGCCTGGTCTGCCTCAGC
GTCCTCCTGTTCCCTGGCCAGCCCAGCCCTGCCCGATGCCTGGCCCAGCAGCCCTTGTCC
CACCTCCCGCTCACGGGCTGCCTGAGCACACTCTTCCTGCAGGCGGCCGAGATCTTCGTG
GAGTCAGAACTGCCTCTGAGCTGGGCAGACCGGCTGAGTGGCTGCCTGCGGGGGCCCTGG

GCCTGGCTGGTGGTGCTGCTGGCCATGCTGGTGGAGGTCGCACTGTGCACCTGGTACCTG
GTGGCCTTCCCGCCGGAGGTGGTGACGGACTGGCACATGCTGCCCACGGAGGCGCTGGTG
CACTGCCGCACACGCTCCTGGGTCAGCTTCGGCCTAGCGCACGCCACCAATGCCACGCTG
GCCTTTCTCTGCTTCCTGGGCACTTTCCTGGTGCGGAGCCAGCCGGGCTGCTACAACCGT
GCCCGTGGCCTCACCTTTGCCATGCTGGCCTACTTCATCACCTGGGTCTCCTTTGTGCCC
CTCCTGGCCAATGTGCAGGTGGTCCTCAGGCCCGCCGTGCAGATGGGCGCCCTCCTGCTC
TGTGTCCTGGGCATCCTGGCTGCCTTCCACCTGCCCAGGTGTTACCTGCTCATGCGGCAG
CCAGGGCTCAACACCCCCGAGTTCTTCCTGGGAGGGGGCCCTGGGGATGCCCAAGGCCAG
AATGACGGGAACACAGGAAATCAGGGGAAACATGAGTGA

SEQ. ID NO: 202

Nucleic Acid Sequence hT1R2

ATGGGGCCCAGGGCAAAGACCATCTGCTCCCTGTTCTTCCTCCTATGGGTCCTGGCTGAG
CCGGCTGAGAACTCGGACTTCTACCTGCCTGGGGATTACCTCCTGGGTGGCCTCTTCTCC
CTCCATGCCAACATGAAGGGCATTGTTCACCTTAACTTCCTGCAGGTGCCCATGTGCAAG
GAGTATGAAGTGAAGGTGATAGGCTACAACCTCATGCAGGCCATGCGCTTCGCGGTGGAG
GAGATCAACAATGACAGCAGCCTGCTGCCTGGTGTGCTGCTGGGCTATGAGATCGTGGAT
GTGTGCTACATCTCCAACAATGTCCAGCCGGTGCTCTACTTCCTGGCACACGAGGACAAC
CTCCTTCCCATCCAAGAGGACTACAGTAACTACATTTCCCGTGTGGTGGCTGTCATTGGC
CCTGACAACTCCGAGTCTGTCATGACTGTGGCCAACTTCCTCTCCCTATTTCTCCTTCCA
CAGATCACCTACAGCGCCATCAGCGATGAGCTGCGAGACAAGGTGCGCTTCCCGGCTTTG
CTGCGTACCACACCCAGCGCCGACCACCACGTCGAGGCCATGGTGCAGCTGATGCTGCAC
TTCCGCTGGAACTGGATCATTGTGCTGGTGAGCAGCGACACCTATGGCCGCGACAATGGC
AGCTGCTTGGCGAGCGCGTGGCCCGGCGCGACATCTGCATCGCCTTCCAGGAGACGCTGC
CCACACTGCAGCCCAACCAGAACATGACGTCAGAGGAGCGCCAGCGCCTGGTGACCATTG
TGGACAAGCTGCAGCAGAGCACAGCGCGCGTCGTGGTCGTGTTCTCGCCCGACCTGACCC
TGTACCACTTCTTCAATGAGGTGCTGCGCCAGAACTTCACGGGCGCCGTGTGGATCGCCT
CCGAGTCCTGGGCCATCGACCCGGTCCTGCACAACCTCACGGAGCTGGGCCACTTGGGCA
CCTTCCTGGGCATCACCATCCAGAGCGTGCCCATCCCGGGCTTCAGTGAGTTCCGCGAGT
GGGGCCCACAGGCTGGGCCGCCACCCCTCAGCAGGACCAGCCAGAGCTATACCTGCAACC

AGGAGTGCGACAACTGCCTGAACGCCACCTTGTCCTTCAACACCATTCTCAGGCTCTCTG
GGGAGCGTGTCGTCTACAGCGTGTACTCTGCGGTCTATGCTGTGGCCCATGCCCTGCACA
GCCTCCTCGGCTGTGACAAAAGCACCTGCACCAAGAGGGTGGTCTACCCCTGGCAGCTGC
TTGAGGAGATCTGGAAGGTCAACTTCACTCTCCTGGACCACCAAATCTTCTTCGACCCGC
AAGGGGACGTGGCTCTGCACTTGGAGATTGTCCAGTGGCAATGGGACCGGAGCCAGAATC
CCTTCCAGAGCGTCGCCTCCTACTACCCCCTGCAGCGACAGCTGAAGAACATCCAAGACA
TCTCCTGGCACACCGTCAACAACACGATCCCTATGTCCATGTGTTCCAAGAGGTGCCAGT
CAGGGCAAAAGAAGAAGCCTGTGGGCATCCACGTCTGCTGCTTCGAGTGCATCGACTGCC
TTCCCGGCACCTTCCTCAACCACACTGAAGATGAATATGAATGCCAGGCCTGCCCGAATA
ACGAGTGGTCCTACCAGAGTGAGACCTCCTGCTTCAAGCGGCAGCTGGTCTTCCTGGAAT
GGCATGAGGCACCCACCATCGCTGTGGCCCTGCTGGCCGCCCTGGGCTTCCTCAGCACCC
TGGCCATCCTGGTGATATTCTGGAGGCACTTCCAGACACCCATAGTTCGCTCGGCTGGGG
GCCCCATGTGCTTCCTGATGCTGACACTGCTGCTGGTGGCATACATGGTGGTCCCGGTGT
ACGTGGGGCCGCCCAAGGTCTCCACCTGCCTCTGCCGCCAGGCCCTCTTTCCCCTCTGCT
TCACAATTTGCATCTCCTGTATCGCCGTGCGTTCTTTCCAGATCGTCTGCGCCTTCAAGA
TGGCCAGCCGCTTCCCACGCGCCTACAGCTACTGGGTCCGCTACCAGGGGCCCTACGTCT
CTATGGCATTTATCACGGTACTCAAAATGGTCATTGTGGTAATTGGCATGCTGGCCACGG
GCCTCAGTCCCACCACCCGTACTGACCCCGATGACCCCAAGATCACAATTGTCTCCTGTA
ACCCCAACTACCGCAACAGCCTGCTGTTCAACACCAGCCTGGACCTGCTGCTCTCAGTGG
TGGGTTTCAGCTTCGCCTACATGGGCAAAGAGCTGCCCACCAACTACAACGAGGCCAAGT
TCATCACCCTCAGCATGACCTTCTATTTCACCTCATCCGTCTCCCTCTGCACCTTCATGT
CTGCCTACAGCGGGGTGCTGGTCACCATCGTGGACCTCTTGGTCACTGTGCTCAACCTCC
TGGCCATCAGCCTGGGCTACTTCGGCCCCAAGTGCTACATGATCCTCTTCTACCCGGAGC
GCAACACGCCCGCCTACTTCAACAGCATGATCCAGGGCTACACCATGAGGAGGGACTAG

SEQ. ID NO: 203

Nucleic Acid Sequence rT1R3

ATGCCGGGTTTGGCTATCTTGGGCCTCAGTCTGGCTGCTTTCCTGGAGCTTGGGATGGGG
TCCTCTTTGTGTCTGTCACAGCAATTCAAGGCACAAGGGGACTATATATTGGGTGGACTA
TTTCCCCTGGGCACAACTGAGGAGGCCACTCTCAACCAGAGAACACAGCCCAACGGCATC

CTATGTACCAGGTTCTCGCCCCTTGGTTTGTTCCTGGCCATGGCTATGAAGATGGCTGTA
GAGGAGATCAACAATGGATCTGCCTTGCTCCCTGGGCTGCGACTGGGCTATGACCTGTTT
GACACATGCTCAGAGCCAGTGGTCACCATGAAGCCCAGCCTCATGTTCATGGCCAAGGTG
GGAAGTCAAAGCATTGCTGCCTACTGCAACTACACACAGTACCAACCCCGTGTGCTGGCT
GTCATTGGTCCCCACTCATCAGAGCTTGCCCTCATTACAGGCAAGTTCTTCAGCTTCTTC
CTCATGCCACAGGTCAGCTATAGTGCCAGCATGGATCGGCTAAGTGACCGGGAAACATTT
CCATCCTTCTTCCGCACAGTGCCCAGTGACCGGGTGCAGCTGCAGGCCGTTGTGACACTG
TTGCAGAATTTCAGCTGGAACTGGGTGGCTGCCTTAGGTAGTGATGATGACTATGGCCGG
GAAGGTCTGAGCATCTTTTCTGGTCTGGCCAACTCACGAGGTATCTGCATTGCACACGAG
GGCCTGGTGCCACAACATGACACTAGTGGCCAACAATTGGGCAAGGTGGTGGATGTGCTA
CGCCAAGTGAACCAAAGCAAAGTACAGGTGGTGGTGCTGTTTGCATCTGCCCGTGCTGTC
TACTCCCTTTTTAGCTACAGCATCCTTCATGACCTCTCACCCAAGGTATGGGTGGCCAGT
GAGTCCTGGCTGACCTCTGACCTGGTCATGACACTTCCCAATATTGCCCGTGTGGGCACT
GTTCTTGGGTTTCTGCAGCGCGGTGCCCTACTGCCTGAATTTTCCCATTATGTGGAGACT
CGCCTTGCCCTAGCTGCTGACCCAACATTCTGTGCCTCCCTGAAAGCTGAGTTGGATCTG
GAGGAGCGCGTGATGGGGCCACGCTGTTCACAATGTGACTACATCATGCTACAGAACCTG
TCATCTGGGCTGATGCAGAACCTATCAGCTGGGCAGTTGCACCACCAAATATTTGCAACC
TATGCAGCTGTGTACAGTGTGGCTCAGGCCCTTCACAACACCCTGCAGTGCAATGTCTCA
CATTGCCACACATCAGAGCCTGTTCAACCCTGGCAGCTCCTGGAGAACATGTACAATATG
AGTTTCCGTGCTCGAGACTTGACACTGCAGTTTGATGCCAAAGGGAGTGTAGACATGGAA
TATGACCTGAAGATGTGGGTGTGGCAGAGCCCTACACCTGTACTACATACTGTAGGCACC
TTCAACGGCACCCTTCAGCTGCAGCACTCGAAAATGTATTGGCCAGGCAACCAGGTGCCA
GTCTCCCAGTGCTCCCGGCAGTGCAAAGATGGCCAGGTGCGCAGAGTAAAGGGCTTTCAT
TCCTGCTGCTATGACTGTGTGGACTGCAAGGCAGGGAGCTACCGGAAGCATCCAGATGAC
TTCACCTGTACTCCATGTGGCAAGGATCAGTGGTCCCCAGAAAAAAGCACAACCTGCTTA
CCTCGCAGGCCCAAGTTTCTGGCTTGGGGGGAGCCAGCTGTGCTGTCACTTCTCCTGCTG
CTTTGCCTGGTGCTGGGCCTGACACTGGCTGCCCTGGGGCTCTTTGTCCACTACTGGGAC
AGCCCTCTTGTTCAGGCCTCAGGTGGGTCACTGTTCTGCTTTGGCCTGATCTGCCTAGGC
CTCTTCTGCCTCAGTGTCCTTCTGTTCCCAGGACGACCACGCTCTGCCAGCTGCCTTGCC
CAACAACCAATGGCTCACCTCCCTCTCACAGGCTGCCTGAGCACACTCTTCCTGCAAGCA

GCCGAGATCTTTGTGGAGTCTGAGCTGCCACTGAGTTGGGCAAACTGGCTCTGCAGCTAC
CTTCGGGGCCCCTGGGCTTGGCTGGTGGTACTGCTGGCCACTCTTGTGGAGGCTGCACTA
TGTGCCTGGTACTTGATGGCTTTCCCTCCAGAGGTGGTGACAGATTGGCAGGTGCTGCCC
ACGGAGGTACTGGAACACTGCCGCATGCGTTCCTGGGTCAGCCTGGGCTTGGTGCACATC
ACCAATGCAGTGTTAGCTTTCCTCTGCTTTCTGGGCACTTTCCTGGTACAGAGCCAGCCT
GGTCGCTATAACCGTGCCCGTGGCCTCACCTTCGCCATGCTAGCTTATTTCATCATCTGG
GTCTCTTTTGTGCCCCTCCTGGCTAATGTGCAGGTGGCCTACCAGCCAGCTGTGCAGATG
GGTGCTATCTTATTCTGTGCCCTGGGCATCCTGGCCACCTTCCACCTGCCCAAATGCTAT
GTACTTCTGTGGCTGCCAGAGCTCAACACCCAGGAGTTCTTCCTGGGAAGGAGCCCCAAG
GAAGCATCAGATGGGAATAGTGGTAGTAGTGAGGCAACTCGGGGACACAGTGAATGA

[0253] Also, the following conceptual translations, which correspond to the C-termini of two orthologous pairs of fish T1Rs, are derived from unpublished genomic sequence fragments and provided. Fugu T1RA was derived from accession 'scaffold 164'; Fugu T1RB was derived from accession LPC61711; Tetradon T1RA was derived from accession AL226735; Tetradon T1RB was derived from accession AL222381. Ambiguities in the conceptual translations ('X') result from ambiguities in database sequences.

SEQ. ID NO: 204

T1RA Fugu

PSPFRDIVSYPDKIILGCFMNLKTSSVSFVLLLLLCLLCFIFSYMGKDLPKNYNEAKAIT
FCLLLLILTWIIFTTASLLYQGKYIHSLNALAVLSSIYSFLLWYFLPKCYIIIFQPQKNT
QKYFQGLIQDYTKTISQ

SEQ. ID NO: 205

T1RA Tetradon

FAVNYNTPVVRSAGGPMCFLILGCLSLCSISVFFYFERPTEAFCILRFMPFLLFYAVCLA
CFAVRSFQIVIIFKIAAKFPRVHSWWMKYHGQWLVISMTFVLQAVVIVIGFSSNPPLPYX
XFVSYPDKIILGCDVNLNMASTSFFLLLLLCILCFTFSYMGKDLPKNYNEAKAITFCLLL

LILTWIIFATAFMLYHGKYIHTLNALAVLSSAYCFLLWYFLPKCYIIIFQPHKNTQKYFQ
LS

SEQ. ID NO: 206

T1RB Fugu

KKQGPEVDIFIVSVTILCISVLGVAVGPPEPSQDLDFYMDSIVLECSNTLSPGSFIELCY
VCVLSVLCFFFSYMGKDLPANYNEAKCVTFSLMVYMISWISFFTVYLISRGPFTVAAYVC
ATLVSVLAFFGGYFLPKIYIIVLKPQMNTTAHFQNCIQMYTMSKQ

SEQ. ID NO: 207

T1RB Tetradon

APKSSQRXLRRTRLXLEWDHPMSVALLFFLVCCLLMTSSSAVILLLNINTPVAKSAGGXT
CXLKLAALTAAAMSSXCHFGQPSPLASKLKQPQFTFSFTVCLACNRCALATGHLHFXIRV
ALPPAYNXWAKNHGPXATIFIASAAILCVLCLRVAVGPPQPSQBLBFXTNSIXLXXSNTL
SPGSFVELCNVSLLSAVCFVFSXMGKBLPANYNEAKCVTFSLMVNXISWISFFTVY